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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: Z15399
A;Accession: T05124
A;Molecule type: DNA
A;Residues: 1-377 <BEV>
A;Cross references: UNIPROT:004904; EMBL:AL031018
A;Experimental source: cultivar Columbia; BAC clone F7H19
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dihydrooyotase (EC 3.5.2.3) - Arabidopsis thaliana
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C;Keywords: hydrolase; pyrimidine nucleotide biosynthesis; zinc
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A; Introns: 10/3;
A; Note: F7H19.110
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Best Local &
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                                               YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDWLP 343
                                                                                                                         | KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDF
                        YGLPRNSSKITLKKSPWKVPDVFNFPFGEIVPMFAGETLQWQP
                                                                                                  KKFFLGTDSAPHERSRKESSCGCAGIYSAPIALSLYAKVFDEAGALDKLEAFTSFNGPDF
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Pred. No. 1.5e-113;
41; Mismatches 33;
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Minimum DB Maximum DB

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Searched:

Scoring table:

Title: Perfect score:

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dihydroorotase VCA0925 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82398 R;Sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; I chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio che A;Accession: E82398
A;Status: preliminary A;Molecule type: DNA
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A;Description: catalyzes conversion of N-carbamoyl-L-aspartate into dihydroorotate A;Pathway: pyrimidine nucleotide biosynthesis
A;Note: zinc required for catalytic activity
C;Superfamily: dihydroorotase
C;Koywords: hydrolase; pyrimidine nucleotide biosynthesis; zinc
F;13,15/Binding site: zinc HHS #status predicted
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A; Residues: 1-342 < KAN>
Terrerences: UNIPROT: P74438;
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A;Variety: PCC 6803
A;Datle_ZS-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09
C;ACCession: S76410
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakam
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe,
DNA Res. 3, 109-116, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanoh
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A; Status: nucleic
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Matches 200; Conserv
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                                                                                                                     Clayton, R.A.; Gwinn, M.L.; Do Bass, S.; Qin, H.; Dragoi, I.;
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Yamada, M.; Yasuda
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I.; Sellers,
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A; Diatus Francis DNA
A; Molecule type: DNA
A; Residues: 1-344 < PAR>
A; Cross-references: UNIPROT: Q9JVD6;
A; Cross-references: gerogroup A,
                                                                                                                                                                                                                                              A;Gene: pyrC; NMA0884
C;Superfamily: dihydroorotase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                   probable dihydroorotase (EC 3.5.2.3) NMA0884 [imported] - C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_c;Accession: G8B1934 R;Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; C; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall
                                                                                                                                                                                                                                                                                           A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete DNA sequence of a serogroup A strain of Neisseria A; Reference number: A81775; MUID:20222556; PMID:10761919
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Nature 404, 502-506, 2000
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A;Map position:
C;Superfamily: o
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                                            PEGŚAFEPĹMTĹYĹſDQATPALVREÁKAAGIŸ-AFKĹŶPĀĠAŤTŃŚDSĠŸſDĹF-KLIPŸ
                                                                                                                         LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL
                                                                   PVDSDENPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV
                                                                                                      LTITREDDMHLHLRDGDALKAVAPYTARQMGRAVIMENLKEEVVSVADALAYKARIMAAL
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Pred. No. 1.4e-73;
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Pred. No. 3e-78
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strain Z2491
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Mungall, K.; Qua
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A;Accession: HBI171
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <TETP
A;Cross-references: UNIPROT:Q9K0D1; GB:AE002422;
A;Cross-references: UNIPROT:Q9K0D1; GB:AE002422;
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0682
C;Superfamily: dihydrooropage
T10453
dihydroorotase (
jSpecies: Pseuc
C;Date: 16-Jul-1
C;Accession: T10
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H81171
dihydrocorotase NMB0682 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2
C;Accession: H81171
C;Accession: H81171
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
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Best Local
   Species: Pseudomonas aeruginosa;Date: 16-Jul-1999 #sequence_revision;Accession: T10453; E83204
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                                                                                                                                                                                                                                                                                             LVLEAGDN-VAATVTPQHLLLNRNDLLVGGVRPHHFCLPVLKRETHRQALVAAVT-GEKA
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                                                                                                                                                                                     YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW
                                                                                                                                                                                                                        HKFFLGTDSAPHAKSAKENACGCAGMFSAMTAIBLYAEVFEKAGALDKLEAFASKNGARF
                                                                                                                                                                                                                                                                                                                                                                       LEEMAKQGILFLVHGEVTDPEIDIFDREAAFIGRVMKPVLAQVPNLKVVFEHITTAEAAR
                                                                                                                                                 YGIPENTDTITLVKQSQTVPASVPYGDGELVPMRAGGEIGW
                                                         (EC 3.5.2.3) - Pseudomonas aeruginosa
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Pred. No. 1.7e-73;
55; Mismatches 88
                        16-Jul-1999
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                   #text_change
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; Dougherty, B.;
; Pizza, M.
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A;Cross-references: UNIPROT: P72170; EMBL: U73505; NID: g3868711; PID: g3868712 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A;Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Brichta, D.M.; Brown, T.M.; Houghton, J.E.; O'Donovan, submitted to the EMBL Data Library, November 1998 A;Description: PyrC (dihydroorotase) sequence from P. ae A;Reference number: Z17024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: catalyzes conversion of N-carbamoyl-L-aspartate A;Pathway: pyrimidine nucleotide biosynthesis C;Superfamily: dihydroorotase C;Keywords: hydrolase; pyrymidine nucleotide biosynthesis; zinc
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A;Residues: 1-348 <STO>
A;Cross-references: GB:AE004773; G
A;Experimental source: strain PAO1
C;Genetics:
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A; Residues: 1-348 < BRI>
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Best Local Similarity
Matches 188; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYRBAILKSL 62
                                                                                                                                                                                                                                               LEAMAEVGMPLLVHGEVTRAEVDVFDREKQFIDEHLRRVVERFPTLKVVFEHITTGDAAQ
                                                                                                                                                                                                                                                                                                                                  PAASRFEPLMVLYLTDRTSTEEIRTAKASGFVHAAKLYPAGATTNSDSGVTRI-DNIFEA 123
                                                                                                                                                                                                                                                                                                                                                            PVDSDFNPLMTLYLTDTTSPMBIKLARBSQVVFGVKLYPAGATTNSQDGVTDLFGKCLFV
                                                                                                                                                                                                                                                                                                                                                                                                                      LTLLR PDDWHIHLRDGAALANTVGDAARTFGRAIVM PNLVP PVRNAAEADAYRQR I LAAR
                                         LPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW
                                                                                  FFLGTDSAPHARHAKEAACGCAGCYSAYAAIELYAEAFEQRNALDKLEGFASLHGPDFYG
                                                                                                                  FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
                                                                                                                                                               FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR
LPRNTDRITLVREEWQAPASLPFGDFDVVPLRAGETLRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%;

// Score 975; DB 2;
// Pred. No. 6.4e-73;
// 43; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AE004091; NID:g9949672; PIDN:AAG06915.1; GSPDB:GN00
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      341
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K.; Lim,
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dilydroorotase (EC 3.5.2.3) - Escherichia coli (strait N;Alternate names: carbamoylaspartic dehydrase C;Species: Escherichia coli C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #tc;Accession: A25008; A27084; C64849 C;Accession: D.; Sjoberg, R.M.; Lundberg, L.G. Bur. J. Blochem. 160, 77-82, 1986 Eur. J. Blochem. 160, 77-82, 1986 A;Reference number: A91177; MUID:87030260; PMID:287688 A;Accession: A25008
                                                                                                                                                                                                                                                                                                                             (strain
                                                                                                                                                                                                              #text_change 09-Jul-2004
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K-12)

ral gene for dihydroorotase PMID:2876892

of.

Escherichia

O

PID:94260

A; Molecule type: DNA A; Residues: 1-348 < BAC>

A;Cross-references: UNIPROT:P05020; EMBL:X04469; NID:g42605; PIDN:CAA28157.1;

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dibydro-orotase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: D85668 C;Accession: D85668 R;Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.;
                                                                                                                                                                                                                                                                              RESULT 8
                              iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterphenous control of the control of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 23 min C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000207; GB:U00096; NID:g1787293; PIDN:AAC74146.1; PID:g1787301 A;Experimental source: strain K-12, substrain MG1655 C;Comment: The de novo synthesis of UMP, the precursor of all pyrimidine nucleotides, i ressed primarily by a cytidine nucleotide.
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Experimental source: strain K-12
R, Wilson, H.R.; Chan, P.T.; Turnbough Jr., C.L.
J. Bacteriol. 169, 3051-3058, 1987
A; Title: Nucleotide sequence and expression of the pyrc
A,Reference number: A91836; MUID:87250268; PMID:2885307
A;Accession: A27084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: pyrc
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A; Residues: 1-348 <BLAT>
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Best Local S
Matches 189
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A; Residues: 1-348 <WIL>
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;17,19/Binding site: zinc (His) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPĽGTDŠÁPHARHRKÉSSCGCÁGCFNÁPTÁLGSVÁTVPÉEMNÁLQHFÉÁPCSVNGÞQFYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR
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sequence of enterohemorrhagic Escherichia
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Pred. No. 1.4e-72;
6; Mismatches 102;
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                                                  J.D.; Rose, D.J.;
Potamousis, K.; Ap
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                                                     Apodaca
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A;Gene: ECB1440
C;Superfamily:
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A,Residues: 1-348 <HAY>
A,GOSB-References: UNIPROT:Q8X8N8; GB:BA000007; PIDN:BAB34863.1;
A,Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dihydro-orotase [imported] - Escherichia coli (strain O157:H7, substrain RII C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90808
R;Hayashi, T.; Wakino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, Jgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, I
                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90808
                                                                                                                                                                          Query Match
Best Local S
Matches 189
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A;Accession: D85668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <STO>
A;Cross-references: UNIPROT:Q8X8N8; GB:AE005174;
A;Experimental source: strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: pyrc
C;Superfamily: dihydroorotase
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Best Local
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                                                                                                                                                                                                                                                                       EC81440
                  83
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa,
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                                                                                                                                                                                           Similarity
PAGHDFTPLMTCYLTDSLDPNELERGFNEGVFTAAKLYPANATTNSSHGVTSV-DAIMPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL 62
                                                                                                     LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYRBAILKSL
                                 PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                              ĽKÍRRÞÓÐMHLHLRÐGÐMLKTVVPYTSEIYGRÁÍVMÞNLAÞÞVTTVBÁÁVÁÝRQRÍLHAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVDSDFNPLMTLYLTDTTSPMBIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV
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                                                                                                                                                                      Conservative
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                                                                                                                                                                    46;
                                                                                                                                                            Score 970; DB 2; 1
Pred. No. 1.7e-72;
6; Mismatches 102;
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Pred. No. 1.7e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g12514597; PIDN:AAG55808.1; GSPDB EDL933
                                                                                                                                                                                                  Length 348
                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                               PID:g13360904; GSPDB:G
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A;Molecule type: DNA
A;Residues: 1-348 < KUR>
A;Cross-references: UNIPROT:Q8ZFU4; Gi
C;Genetics:
A;Gene: pyrC
C;Superfamily: dihydrooxotase
C;Keywords: hydrolase
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APO193
APO193
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AFO193
C;Acc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182
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milarity 53.4%;
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Pred. No. 2.4e-71;
56; Mismatches 100;
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                #text_change 18-Nov-2002
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C;Accession: AF2625
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, D; Kanp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: pyrC
A;Map position: circular chromosome
C;Superfamily: dihydroorotase
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A;Cross-references: GB:AE008688; PIDN:AAL41420.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AF2625
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1937407

dihydroorotase (dhoase) [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: E97407

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                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-393 <KUR>
A;Cross-references: GB:AE007869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
                                                                                                                         A;Gene: AGR_C_703
A;Map position: circular chror
C;Superfamily: dihydroorotase
                                                                                                                                                                                                                                                                                                                                                                               A; Title: Genome Sequence of A; Reference number: A97359; A; Accession: E97407
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Similarity 54.7%;
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; Pred. No. 7.3e-71;
51; Mismatches 95
                                                                                                                                                                                                                                                            PIDN: AAK86214.1;
         Score 951; DB 2;
Pred. No. 7.3e-71;
Sl; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
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                                                                                                                                                                                                                                                                PID:g15155315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dihydroorotase (EC 3.5.2.3) [imported] - Salmonella enterica subsp. enterica serovar (5)Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: ADD638
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: STY1201
C;Superfamily: c
C;Keywords: hydi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL513382;
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                                                                                                                                                                                                                                                                                                                                                                                              ;Superfamily: dihydro;
;Keywords: hydrolase
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Best Local
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APLGTDSAPHSRHRKETRCGCAGCFNAPSALGSYAAVFEEMNALAHFEAFCSLNGPOFYG
                           FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
                                                                              FVESCTEGFVAATVTFQHLVLNRNSLFQGGLQPHNYCLFVLKREIHREALVSAVTSGSKR
                                                             YVRDGSYN-LÄÄTITPOHLMFNRNDMLVGGIRPHLYCLPILKRNIHOOALRDLVASGFTR
                                                                                                                                                                                                                                                                            LSITQPDDWHLHLRDGDVLKAVVSHSAHHEGRAIVMPNLKPPITTTAAAVAYREAILKSL
                                                                                                                           LERMEKLGMPLLVHGEVTHADVDIFDREARFIDTVMEPLRORLTALKVVFEHITTKDAAQ
                                                                                                                                             LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMBHVTTIDAVK 182
                                                                                                                                                                                          PAGHDFTPLMTCYLTDSLDADELERGFHEGVFTAAKLYPANATTNSSHGVTSV-DAIMPV
                                                                                                                                                                                                                lkírr podmívhledgomlkt výpytsetygrát vmpnlaspittvodáatayrorildav
                                                                                                                                                                                                                                                                                                                                                                                                              dihydroorotase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPRNNSKIKLSKTPWKV--PESFSYASGDII---PMFAGEMLDW 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFLGTDSAPHVDPLKECACGCAGIYTSINTMSCLAHVFEDENALDKLEAFASLNGPAWYG
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                                                                                                                                                                                                                                                                                                                               49;
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                                                                                                                                                                                                                                                                                                                                                         Length 348;
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Salmonella enterica s
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#text_change 23-Mar-2001

of aphids

Buchnera

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A;Crostruces: 1-30 CNBUS
A;Cross-references: UNIPROT:P06204; GB:X03928; NID:947865; PIDN:CAP
A;Experimental source: strain LT2
C;Comment: The de novo synthesis of UMP, the precursor of all pyrin
ressed primarily by a cytidine nucleotide.
C;Genetics:
A;Gene: pyrC
A;Map position: 23 min
C;Function:
A;Pathway: pyrimidine nucleotide biosynthesis
A;Pathway: pyrimidine nucleotide biosynthesis
A;Note: zinc required for catalytic activity
C;Superfamily: dihydroorotase
C;Keywords: homodimer; hydrolase; pyrimidine nucleotide biosynthesis
F;17,19/Binding site: zinc (His) #status predicted
RESULT 15
G84968
G194968
dihydrocrotase (EC 3.5.2.3) [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-M
C;Accession: G84968
R;Shigenobu, S; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of a;
A;Reference number: A84930; MUID:20445173; PMID:10993077
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Bur. J. Blochem. 157, 335-342, 1986

A/Ittle: Cloning and structural characterization of the
A/Reference number: A27143; MUID:86220211; PMID:2872051

A/Accession: A27143

A/Molecule type: DNA
A/Residues: 1-348 <NEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydroorotase (EC 3.5.2.3) - Salmonell C;Species: Salmonella typhimurium C;Date: 31-Mar-1993 #sequence_revision C;Accession: A27143
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YVRDGND-YLAATITPQHLMENRNDMLVGGIRPHLYCLPILKRNIHQQALRELVASGFTR
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                                                                                                                                                                                                                     LPMNTGWVELVRDEQQIPGNIALADDSLVPFLAGETVRW
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Pred. No. 1.6e-70;
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A;Accession: G84968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: pyrC; BU334
C;Superfamily: dihydroorotase
C;Keywords: hydrolase
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                                                                     242 RFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFY 301
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                              306 NMPINKETITIIKKPCKIIKKINVGRNVIIPFLSGEILNW 345
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Search completed: February 12, Job time : 29 secs

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Maximum DB seq length: 200000000
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22.2 208524
22.1 1071
22.1 149082
21.8 110000
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10869.499 Million cell updates/sec
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          AX088927 Sequence
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AX470409 Sequence
AJ251897 Beta vulg
AF000146 Arabidops
AK122010 Oryza sat
D90915 Synechocyst
BX321858 Nitrosomo
AP005085 Vibrio pa
AE016925 Chromobac
AR375107 Sequence
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AR375107 Yersinia
AE013777 Yersinia
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ALIGNMENTS

ORIGIN		CDS	Bource	FEATURES		JOURNAL		REFERENCE AUTHORS		ORGANISM	SOURCE	VERSION	DEFINITION	AX088927 LOCUS	RESULT 1
	/note="unnamed protein product" /codon start=1 /protein id="CAC34708.1" /protein id="CAC34708.1" /protein id="CAC34708.1" /brotein id="CAC34708.1" /brotein id="CAC34708.1" /db xrefi"GI:13397886" /translation="MELSITOPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPP /translation="MELSITOPDDWHLMTLYLTDTTSPMEIKLARESQVVFGVKLYPA ITTTAAAVAXREALIKSLPVUSDENVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRP GATTNSQDGVTDLFGKCLPVLQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRP LVQKFPQLKVVMEHYTTIDAVKFVESCTEGFVAAFVHTVPTQHLVLNRNGLEQGGLQPHNY CLPVLKREIHREALVSAVTSGSKRFFLGTDSAPHDRRKKECSGCGAGIYNAPVALSVY AKVFEKENALDKLEAFTSFNGPDFYGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMF AGEMLDWLPAPL"	/organism="Solanum cuberosum" /mol_type="unassigned DNA" /db xref="taxon:4113" 9.	11271	Location/Qualifiers	BASF AKTIENGESELLSCHAFT (DE)	Patent: WO 0114569-A 1 01-MAR-2001;	Schroeder, M.	I Ehrhardt, T., Stitt, M., Geigenberger, P.L., Loef, I., Zrenner, R. and	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; asterida; lamiida; Solanalea; Solanaceae; Solanum.	Solanum tuberosum	Solanum tuberosum (potato)	AX088927.1 GI:13397685	Sequence 1 from Patent WO0114569.	AX088927 1271 bp DNA linear PAT 17-MAR-2001	

Ralstonia

8

Query Match 100.0%; Score 1271; DB 6; Best Local Similarity 100.0%; Pred. No. 4.8e-313; Matches 1271; Conservative 0; Mismatches 0;

Length 1271; Indels 0;

Gaps

0

1 TIGCAAAAATGGAGCTCTCAATCACACAACCTGATGATTGGCATCTTCATCTCCGTGATG 60

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TGCCAAATTTGAAGCCT

TATTGAAATCTTTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAG TATTGAAATCTTTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTTATTTGACAG

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Sequence
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Score 1271; DB 6;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
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Sugar beet genes involved in stress tolerance
Patent: WO 02052012-A 2 04-JUL-2002;
CropDesign N.V. (BE)
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Pred. No. 1e-153;
0; Mismatches 245;
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732 542

912 722 852 662 792 482

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Submitted (22-DEC-1999) Ros R.,
Biologia Wolecular Y Celular De
VALENCIA, SPAIN
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
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AJ251897.1 GI:17977976
dhoase gene; dihydroorotase.
Beta vulgaris
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Molecular cloning
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                  /gene="dhoase"
/codon_start=1
/product="dihydroorotase"
/protein_id="CAC80990.1"
/protein_id="CAC80990.1"
/brotein_id="CAC80990.1"
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/db_xref="GO:18700; CBVXS9"
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LIQKLPQLKVVMEHITTADAVKFIESCNGGNVAATVTPQHLVLNRUSLPQGGLQPHNY
CLPVLKREIHRQALVSAVTSGSKQYFLGTDSAPHERRKECSCGCAGIYNSPVALSLY
AKVFEEAGALDKLEAFTSPNGBDFYGLDRNTSKIKLKKEPWKVLERIPPPSGEIIPMF
                                                                                                                                                                                                                                                'gene="
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/mol_type="mRNA"
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                                                                             TATGGGCTTCCTAGGAACACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCC
                                                                                                                      GAAGAGGCTGGTGCCCTTGACAAGTTAGAGGCATTTACAAGCTTTAATGGACCCGATTTC
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                                                                                                                                          GAAAAGGAAAATGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTT
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Pred. No. 5.6e-153;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1362)
2 (bases 1 to 1362)
2 (bases 1 to 1362)
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Submitted (16-APR-1997) Biochemistry
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TTGAAATCTTTACCTGTTGATAGTGATATTCAACCCTCTTATGACACTTTATTTGACAGAT
                                                              CCGAATCTGAAGCCTCCTGTCACCTCCACTGCAGCTGCCATTATTTACCGGAAATTTATC
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/function="catalyzes to form dihydroorotate"
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                                                                                                                                                                                                                                                                                                                                                        LPRNSSKITLKKSPWKVÞDVFNFPFGEIVPMFAGETLQWQPLK"
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/db_xref="GI:2121273"
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Pred. No. 1.2e-138;
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                                AKI22010 GI:37991633
AKI22010.1 GI:37991633
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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   Rice Full-Length cDNA Consortium,
                                                                                                                                                               sequence.
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                                                                                                                                                                             1750 bp mRNA linear PLN 29-OCT-2003 cultivar-group) cDNA clone:J033111101, full
      National Institute of
                                                    Embryophyta; Tracheophyta; a; Poales; Poaceae;
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895 722 835

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602

715 542 655

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URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M.,
Xie,O., Yokomizo,S., Sujiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,O., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
and Genome Exploration Research Group in Riken Genomic Sciences Center
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RS Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, W., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Ida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Katoh, H., Kawagashira, N., Kabai, J., Kawamata, M., Kikuchi, S., Kishikawa, K., Kishikawa, M., Itoh, M., Kogawa, I., Kishikawa, K., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Koda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Natsuhara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Natuna, K., Numasaki, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Otay, C., Choo, Y., Ryu, R., Saitch, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shiraki, T., Shishiki, T., Sogabe, Y., Tagami, M., Shinagama, A., Shiraki, T., Shishiki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Yokomizo, S. and Yoshimura, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission

Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchienias.affrc.go.jp, 782:81-29-838-7007)

Tel:81-29-838-7007, Fax:81-29-838-7007)
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MEDLINE PUBMED REFERENCE

TITLE JOURNAL

JOURNAL REFERENCE AUTHORS TITLE

TITLE

JOURNAL

COMMENT

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Matches 734;
731 AAGATTTTTTCTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAAAAAGAGTGTTCTTG
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Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.
Ota,Y., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
                                                                          AGTACTGAĀĀĀĠĀĠĀĀĊTĊĀTĀĠĀCĀĀĠĊĀĀŤTGTĠTCTĠĊĠGTĀĀĊĀĀGTĠGĠĀĞTĀĀ
                                                                                                         AGTCCTCAAAAGAGAGATCCACAGGGAGGCACTTGTGTCAGCTGTAACAAGTGGAAGTAA
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                                                                                                                                                                                                           TGTTTTGAACAGGAATTCTCTCTTCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCC
                                                                                                                                                                                                                                                                           TAACTTCGTAGAATCATGCAAAGAAGGTCATGTTGCTGCAACGGTGACTCCCCAACATCT
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="J033111I01"
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Pred. No. 5.1e-129;
0; Mismatches 308;
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                                                                                                                                                                                                                      Direct Submission

Direct Submission

Direct Submission

Submitted (28-JUN-1996) Satoshi Tabata, Kazusa DNA Research

Institute, The First Laboratory for Plant Gene Research; Yana

1532-3, Kisarazu, Chbba 292-0812, Japan

(E-mail:tabata@kazusa.or.jp, URL:http://www.kazusa.or.jp/cyano/,

Tel:81-438-52-3933 (ex.2330), Fax:81-438-52-3934)

Potential protein coding regions were assigned on the basis of

similarity search of the ORFs and GeneMark analysis.
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Synechocystis sp. PCC 6803 DNA,
2137259-2267259
D90915 AB001339 BA000022
D90915.1 GI:1653604
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Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC8803. I. Sequence features in the 1 Mix region from map positions 64% to 92% of the genome DNA Res. 2 (4), 153-166 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada, M., Yasuda, M. and Tabata, S. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions DNA Res. 3 (3), 109-136 (1996)
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Synechocystis sp. PCC 6803
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 130001)
                                                                                           /organism="Synechocystis
/mol_type="genomic DNA"
/strain="PCC6803"
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913 GGCTTCCTAGGAACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAAT 972
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                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTGAACAGGAATTCTCTTTCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCCAG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTTGTTTTATCTGCTAATAA-----TATTGCAGCCACTATTACGCCCCAACATTTAC 20781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAAAĀĀTTTĊĊĊĊGGĊTĠĊĊĠĠŦĀĠŦĠĊŦĠĠĀĀĊĀŤĀŤŦĀĊŦĀĊŦŦĊĀĠĀŤĠĊĀĠŤĠĊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTTTGTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCACAACAACATCTTG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GÍBÁTATTGÁTATTTTCGÁCCGAGAÁÁÁAGTÁTTCATTGÁÁÁAATATTTÁÁTTCCTCTCA 20667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTGGCAGCCATGGAACÁGGTGGÁCTTGCCCCTATTACTCCÁCGGCGÁAGTAÁCGGÁCA 20607
                                                                                                                                                                                                                             TCTCGGCACTGATAGTGCTCCCCACGCTCGCAATAGTAAAGAGAGTTTATGTG
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gene Sgo

912 21081

852

21021

792

20901

20961

732

20841

20727

Sab

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TTCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGGTTACTAATC 432
                                            CTGGAĞCCACCAATTCTGACTTTGĞCGTCACGGA---TATCCATCGATGTGATGCAĞ
                                                                              CTGGTGCCACGACAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAG
                                                                                                                             CCGAAGAAATTATTGCGGCCAAAGCATCCCAGTTTGTTAAAAGCAGTAAAATACTATCCCG
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                                                                                                                                                                                                              TACCTGCGGGAGGCCAGTTTGAACCGCTGATGACCCTTTATCTAACGGATAATACTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                           TACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTC 252
                                                                                                                                                                                                                                                                                               AGCCTCCGGTGCGTTCCGTGGCTGATGCCGCCGCCTATCGGGAAAGGATTCTCGCCGCCA 20370
                                                                                                                                                                                                                                                                                                                              AGCCTCCTATCACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTT 192
                                                                                                                                                                                                                                                                                                                                                                                    AAGCAGTTCTACCCCACACTGTCCGTCAATTTGCTAGGGCGATCGTCATGCCCAATTTGA
                                                                                                                                                                                                                                                                                                                                                                                                           AGGCAGTTGTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTTACCATCACTCGACCCGACGACTGGCACCTGCATCTACGGGATGGAGCGGCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTCTCAATCACACAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 345.6; DB 1;
Pred. No. 3.3e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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JOURNAL
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FEATURES
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ORGANISM
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BX321858
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ACCESSION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21082 AATTGCCCCGTAATACAGCACAAATTACGTTGATGAAAAACCCCTTGGCGTATTCCTGCTG 21141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ### 306050 bp Nitrosomonas europaea ATCC 19718, BX321858 AL954747 BX321858 J GI:30180174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nitrosomonas europaea ATCC 19718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-NOV-2002) Submitted on behalf of the Nitrosomonas genome consortium, the DOE Joint Genome Institute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hooper,A., Klotz,M., Norton,J., Sayavedra-Soto,L., Arciero,D., Hommes,N., Whittaker,M. and Arp,D. Complete Genome Sequence of the Ammonia-Oxidizing Bacterium and Obligate Chemolithoautotroph Nitrosomonas europaea
J. Bacteriol. 185 (9), 2759-2773 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chain, P., Lamerdin, J., Larimer, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTTTTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGA 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arimerfw@ornl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 306050)
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                                                                                                                                                                                                                                                                                            TLRAIYDASLALAKQLNMEAVAEGVEDREDWELLRQTGCDLAQGNFISRPMPAEALGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tag="NE0566"
                                                                                                                     tag="NE0567"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTTKKCHVKSI HELLWFLRGETHIJYLKRNGVSI WDEWADENGDLGEF VGHOWRSWA ASDGTVIDQISQVIQQI KETPDSRRMI VSAWNVGDLDKWKLAPCHVLFQFYVADGRLS CQLYQRSADI FLGVPFNI ASYSLLTLMI AQCCDLQPGEFVHTGGDAHLYLNHLEQARL QLEREPRALPAMQLNSTVRNI FDFGYEDFTLHDYDPYPPI KAPVAV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="InterPro IPR000819:IPR001589:IPR001687 COGs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MYQYLDLMRHVLQYGHKKSDRTGTGTLSVFGYQMRFDLQTGFPL
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/note="1 probable t
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                             Similarity
  AGGCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGA 132
                                                     AGCTGACTTTTACCCGTCCGGATGACTGGCACCTGCATTTGCGTGACGGTAACGCCATGC 171850
                                                                                         AGCTCTCAATCACACAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTA 72
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not experimental
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RQLVKLAIFVANIDPNLTFIIQNELFIGLNTVSNPGFISRGFDQNRAFVGLGYKVHQN
ATVELGYMNOFIDRRHNPRDDQMMHNFAVNLFLNF"
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/locus_tag="NE0572"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="NE0572"
                                                                                                                                                                                                 23.1%; 57.4%;
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                                                                                                                                                                Score 294.2; DB 1; Length 306050;
Pred. No. 4e-64;
0; Mismatches 428; Indels 12;
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DEFINITION
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AP005085 303450 bp DNA Vibrio parahaemolyticus DNA, chromosome 2, AP005085 BA000032

complete sequence,

BCT 07-APR-2004 sequence, 2/6.

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GCTGGAAACTGGC 172817
                                     ACTGGTTGCCGGC 1039
                                                                                                                              TCTATGGTTTACCACGTAATACCGATCGGATTTCCCTGATCAGGGAAAGCTGGCAGATTC 172744
                                                                                                                                                                                                                                                                                                                                ATTCCAGATTCTTCCTTGGTACCGACAGCGCACACATCCGGTCAGAGACAAAGAATCAG 172564
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                                                                                            CCGAATCCTTTTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCG 1026
                                                                                                                                                              TTTATGGGCTTCCTAGGAACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTAC 966
                                                                                                                                                                                                                                                              CCTGTGGGGTGTGCGGGTATTTACAGTGCTCATGCAGCCATCGAATTTTATGCCGAGGTAT 172624
                                                                                                                                                                                                TCGAACAGGCTGGCCGGCTCGATCGACTGGAGGCTTTTACCAGGCTTTTCACGGCCCCGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTGATGCTGAACCGGAATGCCCTGTTTACCGGCGGATTGCGTCCGCATCATTACTGTT 172444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGTCGAGTTTGTGCAGAC---GGCTCCAAACCGGATTGCTGCCACGATTACCGCACACC 172384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTT 192
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Tagomori,K., Iijima,Y., Najima,M., Nakano,M., Yamashita,A.,
Kubota,Y., Kimura,S., Yasunaga,T., Honda,T., Shinagawa,H.,
Hattori,M. and Iida,T.
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V cholerae
Lancet 361 (9359), 743-749 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This work was done in collaboration with Kozo Makino, Ken Kurokawa, Katsushi Yokoyama, Takayuki Uda, Kenichi Tagomori, Masatomo Najima, Masayuki Nakano, Yoshino Kubota, Shigenobu Kimura, Teruo Yasunaga, Takeshi Honda, Hideo Shinagawa, Tetsuya Iida (Gsaka University), Yoshio Iijima (Kobe Institute of Health), and supported by the Research for the Future Program of the Japan Society for the Promotion of Science. This clone was isolated from a patient presenting with acute gastroenteritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanagawa 228-855, Japan
(E-mail:hattoriogenome.ls.kitasato-u.ac.jp,
URL:http://genome.ls.kitasato-u.ac.jp/, Tel:81-42-778-8194,
Fax:81-42-778-8193)
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J. Clin. Microbiol. 38 (6), 2156-2161 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AP005085.1 GI:28808465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-APR-2002) Masahira Hattori, Kitasato Institute for Life Sciences, Kitasato University; Kitasato 1-15-1, Sagamihara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 303450)
Hattori, M., Yamashita, A., Oshima, K. and Shiba, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrionaceae; Vibrio.
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                                                                   /translation="mulkavprallvillasslpissyayaapnanesslvqqowegn
wptoneaeklvoraisayyomopamnyigmrdoseskergynvlpiwkdrmd
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RGGLYLLLppnydgpvpkgyfyfissynnvlpipfrtmymkkgengadpsbavkiaegyr
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81. .1574
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                                                                                                                                                                                                                                                                                                     /product="hypothetical signal peptide protein"
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identity 68 in 487 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DNA"
strain="03:K6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Vibrio parahaemolyticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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.2314)
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SgS

complement (1835.

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/evidence=not_experimental
/transl_table=11
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/protein_id="BACG1648.1"
/db_xref="GI:28808471"
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/gene="VPA0302"
/note="similar to GB:AAA64344.1 (L16865) percent identity
52 in 129 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/evidence=not_ex
/transl_table=11
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2974. .3714
/gene="VPA0303"
/note="similar to GB:AAL20622.1 (AE008775) percent
identity 54 in 243 aa"
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sfesgarlelmsmegvttcenshsmqvtglahfafalgseqavdqitktlvedgyqri
dgfrytgdgyyescvldpdgnrieltv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VPA0302"
2493. .2882
                                                                                                                                                                                                 /gene="VPA0305"
4319. 5860
/gene="VPA0305"
/note="similar to REF:NP_231225.1 (NC_002505) percent
identity 83 in 510 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mnprqneilqlvndrkrvqvtelsdiigvsgvtirqdlnfleqq
Gylkrvhgaatalqsddidtrlevrfdikqtlankaadlvafnetvlieggsanalla
Rtlaergdvtiitpsayiahlirntsaniillggvyqhqgeslvgpltklcienihfs
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QGLDGGFYSAEQVSQTSNGAALLVFYSSDIHATLEKVAKFGGQIIRPIFEFPGGCRFH
FTEPSGNEFAVWSESH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (3733. .4089)
/gene="VPA0304"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2493.
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/transl_table=11
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/note="similar to DBJ:BAB43758.1 (AP003138) percent
identity 57 in 158 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISVLLTDKAAPKSDLEQLKKLGVEVVLG"
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/db_xref="GI:28808469"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
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'protein_id="BAC61644.1"
/translation="mysthwratmqmsksfllityglastslqaqtltrdngapygdn
Qnsitagengsvllqdvhliqklqrfareripervyhargtgahgefyasgdfsbltv
                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
/protein_id="BAC61647.1"
/db_xref="GI:28808470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GB:AAF96321.1 (AE004376) percent
identity 76 in 117 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (3733. .4089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAFLGIDGFHQDTGFTSRDMMRADIAEAILAKKRRNIVLTDSSKFGQIYPSSIGKTNE
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/db_xref="GI:28808467"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="VPA0304"
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Query Match 22.9%;
Best Local Similarity 57.4%;
Matches 584; Conservative
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ATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCT
                                            CACGGCGA---ACAATTCGAACCTCTGATGGCGCTTTACCTAACCGATAACACCACGCCA 104108
                                                                               CCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTCCT
                                                                                                                                                                                                                                                                                                                       CCACCTGTTACCAATACCGAAATGGCACTTGCCTACCGCGATCGAATTCTGAAAGAGCAG
                                                                                                                                                                                 CCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTTTA 194
                                                                                                                                                                                                                                GCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAAG
                                                                                                                                                                                                                                                                                                                                                       CTCTCAATCACAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTAAG 74
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5962. .6429
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(complement (6548. .7201)
/gene="VPA0307"
complement (6548. .7201)
/gene="VPA0307"
/gene="VPA0307"
/gene="VPA0307"
/gene="VPA0307"
/gene="VPA0307"
/gene="VPA0307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (7234. .7959)
/gene="VPA0308"
complement (7234. .7959)
/gene="VPA0308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTVRVNYQTTAVIDVDPEKGFSELCPDELPVAGALDIVPELLKNHKKGEKKLVSRDLHPPKAAWDAETPANMLEPVGLPNVDVKWNRHCVLGTTGVELLDGLPVLDTVDPQVNKGMDPDAHPYGIFFHDVADTKTTGANEFLKCNKIDTVVVGGLALDFCVKKSVMQALDLGFKVIVNLAATRAVLPDTVDSVIAENKKGALFVKNADDIIVERFA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to GB:AAF96011.1 (AE004352) percent dentity 60 in 241 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative pyrazinamidase/nicotinamidase"
/protein_id="BAC61650.1"
/db_xref="GI:28808473"
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/transl_table=11
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IRDSI KFPDMVISLKESBVTUNQDPNRFFDFFSHEPSATHMLTWYSNIGTPASYRTM
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RGNYFKWDLYVKVLSPERLSKLDYNGLDATKVWLNVPDRKVGTWTLNRLPENFFLETE
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RSMNEQDRSDLIANLAGDLNKVIDKDIKATMVSYFYRADKEYGSRLAEATDTNLSQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="AnkB protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5962. .6429
/gene="VPA0306"
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Pred. No. 3.3e-63;
D; Mismatches 424;
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KEYWORDS
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AE016925/c
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                               Brazilian National Genome Project Consortium
The complete genome sequence of Chromobacterium violaceum reveals
remarkable and exploitable bacterial adaptability
Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11660-11665 (2003)
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                                                                                                                                                  Chromobacterium violaceum ATCC 12472
Chromobacterium violaceum ATCC 12472
Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                           complete genome.
AE016925 AE016825
AE016925.1 GI:341
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Chromobacterium violaceum
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FEATURES
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="bioA"
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3845. .4963
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/transl_table=11
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located using_Glimmer/Blastx"
                                complement (6173. .6757)
/locus_tag="CV4214"
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/note="identified by sequence similarity; putative;
/ocated_using_Glimmer/GeneMark/Blastx/COG3575"
                                                                                                                                                    /locus_tag="CV4214"
                                                                                                                                                                                                                                                                LKDLDVKSRRELNRLWSQVKIGR"
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/note="identified by sequence similarity; putative; ORF
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   CAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTAAG
                                                            GAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGTG
                                                                                                                                                                                                                                   GACGAAATCCGCAAGGCCAAGGCCTGCGGCTTCGTCCACGGCGTCAAGCTGTACCCGGCC 130031
                                                                                                    CTGGÁGGCGÁTGGCCGAAGCCGGCATGCCGCTCTTGGTGCÁCGGCGÁAGTCÁCCGÁCGCC
                                                                                                                                                                  GGCGCCÁCCACCAATTCCGACCACGGCGTCÁCCGATAT---CGCCCACGCGATGCCGGCG 129974
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                                                                                                                               CTACAAGAAATGGTTGAGCATAATATGCCTTCTTGCTTGATGGAGAGGTTACTAATCCT 434
                                                                                                                                                                                                 GGTGCCACGACAAATTCTCAAGATGGAGTGATCTTTTTCGGGGAAGTGTTTACCAGTT 374
                                                                                                                                                                                                                                                            ATGGAAATCAAACTAGCAAGAGAGAGGAGGCAAGTTCGTATTTTGGGGTGAAGGTTGTACCCTGCT 314
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(product=in_id="AAQ61875.1"

/protein_id="AAQ61875.1"

/db_xref="g1:34105521"

/translation="MIETDKLFGAAPERRIVTPQRASEQEEALERALRPKLLDEYVGQ
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DLPFTLVGATTRAGMLTNPLKDRFGIVARLEFYNAEELTRIVSRSAGLLNVQLSDDG
AFEVAKKSGTTRRIANRLLRRVRDYAEVKSDGVVTMAVADAALAMLDVDPAGLDVMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="CV4216"
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located using GeneMark/Blastx/COG0108"
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/note="identified by
located using Blastx"
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protein_id="AAQ61874.1"
/db_xref="GI:34105520"
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                              135 CCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTTTA 194
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Nucleic acid and amino acid sequences relating for diagnostics and therapeutics Patent: US 6605709-A 113 12-AUG-2003;
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Sequence
AR375107
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
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CCCCCGATCACCATTGAAGCCGCCGTCGTTATCGTGATCGCATAAAAGCAGCTATT 222
                                                                ACCGTTGTTCCTTÄTÄCCAGTCGTTÄTTTTGGCAGAGCTATCGTAÄTGCCAÄÄTCTTGTT 162
                                                                                    GCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAAG 134
                                                                                                                               CTCACTATTCGCCGTCCTGATGATTGGCATGTTCACTTTCGTGATGATGACATGCTAAAA 102
                                                                                                                                                      CTCTCAATCACACCAGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTAAG
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Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn
Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.
Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.
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DNA sequence of both chromosomes of the
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Medical Center Dr, Rockville,
Location/Qualifiers
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complement (4685...5710)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MQCEFFIQKRCTSCHLCAQPYSEQVTNKDQQLRELIAPATDVQW LPPVTSADTAFRIKAKMYVLGAAHAPILGIEDAQGQPLSLVTCTLYPQPMQELLAYLE NHIRIAGIPPYNKLKKKGELKFILLTRSENSGQFMLRFVARSHAVLERIENLPTLIA AFPMIEVISVNIQPHMARALEGEEEIFLTTSGSLLEHFNDVPMVIRPKSFFCTNPKVA EQLYATARTWVREIAPTQMWDLFCGVGFALHCAAPDTAVTGIEIFPEAIASAQRSAQ NPQTMVKDIAELSSYQMIRVGSOMSAPELVLVNPPRRGLGSELTAQLEALAPKYILYSSC NPQTMVKDIAELSSYQMIRVQNFDMFPHTDHAEVLTLLVRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="conserved hypothetical protein"
/protein id="AAF96827.1"
/db xref="GI:58367"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="TrmA family RNA
/protein_id="AAF96826.1"
/db_xref="GI:9658366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identified by sequence
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/gene="VCA0929"
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GB:U00096 SP:P75817 PID:1787083; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (3444. .4571)
/gene="VCA0929"
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AILEGQRIHSDDMVFSTKEERKKVDGYIVSGIAADEGFILNSRRRWISWLLDAEPQVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="G1:9658364"
/translation="MTPLLTAYLQAWKQYFDFSGQTTRDDFWWFMLAHLLITLVVVSI
FIATNUFGWLDLFYSLISFIFMLAILVRRLHDTQRSGWWAWLFVIFVIGFFWLIYLLV
QPSSSHFTDKALLS"
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TTGCAAGCGATGCAGGAAGTCGGTATGTTGCTGTTGGTGCACGGTGAAGTCACCACGCAC
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78; Conservative
                                CTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTGGTTCATGGAGAGGTTACTAATCCT 434
                                                                                    GGTGCGACCACCTCGGATTCAGGCGTCAC---TTCAGCCAAAAACATTTACCCAGTT
                                                                                                                            GGTGCCACGACAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGTT 374
                                                                                                                                                                        GAGGAAATTCGCAAAGCCAAAGCGTCAGGCAAAGTCGTTGCAGCTAAGCTTTÀCCCAGCC
                                                                                                                                                                                                                ATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GATACTGTACGCGÁCÁTCAGCCGTTÁTAACGGCCGCGCGCTGATCÁTGCCTÁÁCACGGTT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement (7773 . 7874)
/gene="VCA0934"
Complement (7773 . 7874)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cold shock domain family protein"
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8246. .8602
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/transI_table=1

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/protein_id="AAF96831.1"

/db_xref="GI.9658371"
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7464. 7676
7964. 7676
/gene="vCA0933"
/note="similar to GB:U00096 PID:1651256 PID:1778540
PID:1786841 PID:833769; identified by sequence similarity;
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/transl_table=
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/gene="VCA0932"
/note="identified
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7101. .7238
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RESULT 13
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Submitted (03-JUL-2003) Submitted on behalf of the Prochlorococcus genome consortium, the DOE Joint Genome Institute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                    Rocap,G., Larimer,F.W., Lamerdin,J., Malfatti,S., Chain,P., Ahlgren,N.A., Arellano,A., Coleman,M., Hauser,L., Hess,W.R., Johnson,Z.I., Land,M., Lindell,D., Post,A.F., Regala,W., Shah,M., Shaw,S.L., Steglich,C., Sullivan,M.B., Ting,C.S., Tolonen,A., Shaw,S.L., Steglich,C., Sullivan,M.B., Ting,C.S., Tolonen,A., Webb, B.A., Zinser,E.R., and Chisholm,S.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prochlorococcus marinus subsp. pastoris str. CCMP1986 (Prochlorococcus marinus MED4)
Prochlorococcus marinus subsp. pastoris str. CCMP1986 Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
                                                                                                                                                                                 2 (bases 1 to 349082)
Larimer, F. and Rocap, G.
                                                                                                                                                                                                                                                                                                                                    Genome divergence in two Prochlorococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome.
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                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                 Nature 424 (6952),
                                                                                                                                                                                                                                                                                                         niche differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGTAAGCTAGAAAATCTGGAAGCGTTCGCTAGCTTTAATGGCCCTGATTTCTACGGC 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAAIGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTTTATGGG 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTTTCTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAAAAGAGTGTTCTTGTGGA 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTANAGCGTGCGACTCACCAACACGCGTTAGTGGCAGCGGCAACCTCTGGCAGCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCAAAAGAGAGATCCACAGGGAGGCACTTGTGTCAGCTGTAACAAGTGGAAGTAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITAACCGTAACCACATGCTGGTTGGCGGTATTCGCCCACATTTCTACTGTTTGCCAATC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAACAGGAATTCTCTCTCCAAGGGGGGCTTACAACCGCATAATTACTGCCTTCCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGTGCAA---CAAGCAGGCGATAACGTTGCGGCAACGATTACCGCGCACCATTTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCACAACATCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGATTTCCCGCAACTGAAAATTGTGCTTGAACACATCACCACCGCCGATGCAGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCCGTTTGGCAGCGATATCGTGGTGCCAATCCGCGCCGGTGAAAATATCGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCGACTGG 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCTAGGAACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAATCC 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGCAGGTTCTTACACAGCCCATGCAGCTCTTGAGTTGTATGCCGAAGTGTTTGAAAAA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGCTGGTATTTACAATGCACCTGTAGCCTTGTCAGTATATGCGAAGGTGTTTGAAAAG 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTTCCTAGGTACGGACTCTGCCCCGCACGCCAAAGGCCGCAAAGAAGCCGCTTGTGGC 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 349082)
                                                                                                                                                                                                                                                                                    1042-1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        674
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                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/transl_table=11
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/product="putative cyanate
/pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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DYLRVSKSLGASKSITIRRVILPAIMENILAGMRISMGTAMLVIVAAEMLLGTGIGYF
INNEWNNLSLENIFVAIIIIGFTGFILDQFFGFLQDKFDYSI"
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coidentity: CCMP1378 = MED4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="PMM0370"
3283. .4968
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/note="Signal predicted
probabilty 0.892) with o
                                                                                                                                                                                                                                                                                                                                            4999. .5088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative cyanate
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4999. .5781
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/evidence=not_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Prochlorococcus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .349082
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/transl_table=11
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503. .2835
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/note="5 probable tra
MHMM2.0"
  'locus_tag="PMM0372"
                                  1ocus_tag="PMM0372"
1798. .6652
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                                                                                     .6652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      start=1
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                                                                                                                                                                                                                   .5082,5212.
                                                                                                                                        transmembrane
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cleavage site
                                                                                                                                                                                                                 .5280,5404.
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                                                                                                                                        helices predicted
                                                                                                                                                                                                                   .5472,5590.
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                                                                                                                                                                                                                                            Complement (7843. .8211)
/locus tag="PMM0376"
complement (7843. .8211)
/locus tag="PMM0376"
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                                       complement (8152. .82 /locus_tag="PMM0376"
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/db_xref="GI:3363965"
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  /note=\signal predicted by SignalP 2.0 HMM (Signal peptide
                                                                                                                                                                                                                     evidence=not_experimental
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7504. .7827
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/note="1 probable trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evidence=not_experimental/
transl_table=11
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/transl_table=11
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Viqbkfgdgimsaidfsievdkvedpkgdrvlvkmcgkflpykkm"
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685. .7128
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C_number="4.2.1.104"
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                                                          .8211)
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Best Local S
Matches 560
187851 CACATAAATAGAAATGCAATGTTCTTTGGAGGTTTAAATAGTGACTTTTACTGCTTACCA 187910
                                                                                                                                                                                                                                                                187680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
                                                                                         GATTTTGTTCAGAGGAATAACTTAGG------
                                  GTTTTGAACAGGAATTCTCTTCTCTTCCAAGGGGGCTTACAACCGCATAATTTACTGCCTTCCA 671
                                                                                                                 AAGTTTGTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCACAACATCTT 611
                                                                                                                                                              ATACĂACĂĂTTCCCĂAGĂTTAĂĂĠATTGTTTTAGĂĞCĂTATAĂCTĂČCTCTTĂTGCAĞTT
                                                                                                                                                                                                   GTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTT
                                                                                                                                                                                                                                          CCTGAAGTAGATATTTTTGÁTAGGGAAGAAGTTTTTTATTGÁTAAGAACTTTCÁCCTTTA 187739
                                                                                                                                                                                                                                                                         CCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTG 491
                                                                                                                                                                                                                                                                                                                             ATTTTTGĀĀGTTĀTGCAAGĀĀCTTGGAĀTĠCĊĀCTTTTAATTCĀTĠĠĀĠĀĀĠTCĀCTGĀC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTCTAATAATTCTACATTTGAGCCATTAATGACGATATATCTTACGGACGAGACAATA 187502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAACCCAATAACATCTATAGAAAAATGTATTTCTTATAAAAATTCTATATTTTGAAGCA 187442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAAATATTATTAGGTTTÁCATCTCÁATATTTTGGTAGGGCTÁTTGTGÁTGCCÁÁÁCACC 187382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATTAACTATATCAAAACCGGATGATTGGCATTTACATTTAAGGGAAGGCATTGTTTTA 187322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/transl_table=11
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complement(8212. .8475)
/locus_tag="PMM0377"
/codn_start=1
/eviden-
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/db_xref="GI:33639668"
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KAMILMSCSDLEKFGSMLEQPELKOMDIDNNCVDTVYNLELIE"
complement (8526, ...8798)
/locus tag="PMM0378"
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Pred. No. 1.3e-60;
0; Mismatches 391;
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551

187679

187799

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RESULT 14
AE013777
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AUTHORS
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SOURCE
ORGANISM
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ACCESSION
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JOURNAL
PUBMED
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Yersinia pestis KIM section 177
AE013777 AE009952
AE013777.1 GI:21958537
                                                                                                                                                                                                                                                                                                                                                                                                       Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G. Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz, Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 10421)
Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G.
Liss, P., Perna, N.T., Rose, D.J., Mau, B., Zhou, S., Schwartz,
Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V.,
Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S.,
Blattner, F.R. and Perry, R.D.
Genome Sequence of Yersinia pestis KIM
J. Batteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                    Submitted (21-FEB-2002) Genetics, Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yersinia pestis KIM
Yersinia pestis KIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCTTCCTAGGAACACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAA
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/function="putative membrane"
/functe="residues 10 to 226 of 232 are 70.96 pct identical
/note="residues 5 to 220 of 308 from GenPept : >gb|ALL23215.1|
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/protein_id="AAM85302.1"
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                                                                                                                                                                                                    gene=
                                                                                                                                                                                                                                     /db_xref="taxon:187410"
                                                                                                                                                                                                                                                                              organism="Yersinia pestis/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                        transl
                                                                                                                                                                                                                                                               strain="KIM"
                                                                                                                                                                                                        Y1734"
                                                        _table=11
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                                    protein'
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Schwartz, D.C.,
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Schwartz, D.C
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1216. .1620
/gene="y1737"
1216. .1620
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/function="unknown"
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LFNISPDDIFSKMVFAGYRFLLAGIVLLLFALLASKALGRLKKGYQQLAILGLTQTA
LQYVFFYIGLAYTTGVKGSINKATGTFFFSVLLAHYLYKBNGTLTLNKIIGCALGFFGW
VVNVGSDLMDFNFSLLGEGSVVLAAFILSAASIYGKRISQTMDTTVMTGYQLAIGGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="unknown"
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/note="residues 10 to 32 of 37 are 60.86 pct identical
residues 711 to 733 of 929 from GenPept : >gb|AAB53936.
(U62023) sensor/regulator protein RpfA [Pectobacterium
Carocovorum subsp. carotovorum]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLGGYLFVFGLGQ"
                                                                                                             /translation="mmsnoflsvtsskdrtytmpvlhnrisnbelkarmlaegerrt"
/srykyftledaktfrdnlysofrykloyfgrvylakeginagisplanifylkaldyn
Ashpaldovelhunaheddaksewlalkoyfgrvylakeginagisplanifylkaldyn
Omiddpdtlfvdmrnhyeyforfkaldynestrifkardinadhiolikeknivmyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLTVCKHAPIKQADLPQADILLLDIRMTLMDGTQVYT" 1216. .1620
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complement(1097.
                                                                                                                                                                                                                                                                                                                      to residues 1
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1925. .3046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           YWQMASLLIVAGIALLAGLITSGFTDHDYRCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="mintlsnkaggrdrlswilisvcrssavdhpvyvvslfqieplr
fvsslntilttrdllegyrhfpmyklsslifirgwtmqaaklsagllatggilgygga
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/protein_id="AAM85305.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      >gb|AAK22204.1|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical"
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/transl_table=11
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/protein_id="AAM85306.1"
/db_xref="GI:21958542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="y1736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="y1735"
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                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                              /gene="y1738"
/note="residues 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="unknown"
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1739"
                                                                                                                                                                                                                                                                                                                      ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 to 122 of 134 are 35.29 to 383 of 699 from GenPept (AE005696) thio:disulfide
                                                                                                                                                                                                                                                                                                                        19 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [Caulobacter crescentus] "
                                                                                                                                                                                                                                                                                                                        o 366 of 373 of 350 from
                                                                                                                                                                                                                                                                                                                        are
                                                                                                                                                                                                                                                                                                                          e 73.85 pct
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                                                                                                                                                                                                                                                                                                                             : identical
B1055"
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gene="y1739" /function="putative transport" /note="residues 10 to 349 of 361 are

60.00 pct identical

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repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="bypothetical protein"
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/db_xref="01:21958544"
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/complement(4825..5466)
/gene="y1741"
/complement(4825..5466)
/gene="y1741"
/function="unknown"
/note="residues 10 to 199 of 213 are 28.71 pct identical to residues 2 to 187 of 199 from GenPept : >gb|AAC46458.1|
/codon graph="y1"
/codon graph="y2"
/codon gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5706. .6821)
/gene="golh"
/note="sylonym: y1742"
complement (5706. .6821)
/gene="golh"
/function="putative"
/note="residues 1 to 371 oresidues 1 to 372 f.
                                                                                                                                                                                                                                              /product="sarcosine oxidase-like protein"
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AGCGILFNCPVTAIESHQAGYDVVTIOTYSAJKVVVTRGTWYKELLPTLPVTPVRKV
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7182. .8390
                                                                                                        /note="insertion element"
/insertion seq="IS285"
7182. .8390
                                                                                                                                                                                                       SGHGFKFATALGEVTALFAQDKPSPIDISAFSLARFR"
                                                                                                                                                                                                                      FGRYAEDGTEVFSFLRHFLPGVGVCLRGEACSYDMSPDEDFIIDTLPEDERVMVVSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl tart=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLSDKDVNHMKILIIDECFYTRSGVNTYLNSVSSIKLMDVPTVE
EATLAIQEFQPDIIIVNLTQYCRYGGHCPLLAQFIHYCTRAKYYIYLDASYFSSTPI
PLTESVSMPIPLTESVSILAKKHLPNLLRRLPGFSLERLGIQPNQQASLFSPQEHKVM
CYMMTEMPNYRIARKLNISGSTVYSHKRHITEKIKVRNRLELCFIYNVFKYLY"
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/db_xref="GI:21958545"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative transport protein"
protein id="AAM83307 1"
/brotein id="AAM83307 1"
/db xref="Gi:21958543"
/translation="MAVWIQGLIMTTPVSNQGLRLVAMLAMLVVIMAGIKAASPIVV
PPLLALFLAIVLNPLVKLLERIKIPRTLAVILLVTIIILLMVLLFGRLGSSLNEFARS
LPQYRGMMLEKORDLQEFALHENIERSVDDIMKYVDBSMANNFVTRLLSHLSGAMTST
FLLLMTVVFMLEEVERWPYKYQLMFDNPEKGNAILKRALNGVTHYLVIKTIISIATGI
YIUHLIAGNIIDPRMGRGLGLAFVLNYIPNIGSVLAAIPPIIQALLFNGFADAFAVTGG
ELTPAGYRFAVLLSDGKPAKVEEEQAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="y1740"
/note="residues 4 to 37
residues 12 to 45 of 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4368. .4481)
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/transl_table=
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/gene="y1740"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 371 are 64.24 pct identical from E. coli K12 : B1059"
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Best Local S
Matches 569
10044 CTGAATGCATTGCAACATCTGGAAGCGTTTTGCGCCTTAAATGGCCCACGATTTTATGGC
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GAAAATGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTTTATGGG 914
                                               TGTGCGGGTGTATTCAACGCCCCAGCGGCATTGCCTGCTTATGCTTCCGTGTTTGAGGAA
                                                                                      TGTGCTGGTATTTACAATGCACCTGTAGCCTTGTCAGTATATGCGAAGGTGTTTGAAAAG 854
                                                                                                                                                                                                                        TTGAAGCGCAGCACCCATCAGCAAGCATTGCGCGCAGCCGTCGCCAGTGGTTCTGATCGC
                                                                                                                                                                  CTCAAAAGAGAGATCCACAGGGAGGCACTTGTGTCTCAGCTGTAACAAGTGGAAGTAAAAGA
                                                                                                                                                                                                                                                                                                        TIGAACAGGAATICICICITCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCCAGTC 674
                                                                                                                                                                                                                                                                                                                                                                                             TATGTGCTGGCAGGCA---ATCGTTTCCTTGGGGCAACCGTCACGCCACAACACTTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCCACAACATCTTGTT 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAAATTTCCACAATTGAAGGTCGTGATGGAGGATGTTAACCACCATTGATGCTGTTAAG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAAAGTTTCCCCGAACTAAAAATTGTCTTTGAGCATATCACGACCAAAGATGCGGCAGAT 9746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGTT 374
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//note="IS285; residues 1 to 402 of 402 are 100.00 pct
identical to residues 1 to 402 of 402 from GenPept:
-gb|AAC13227.1| (AF053947) transposase [Yersinia pesti
/codon start=1
/transl table=11
/product="putative transposase"
/protein_id="AAM85311.1"
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1.1e-59;
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CATCTCCGTGATGGTGATGTTCTTA	GATGATTGG	CTCTCAATCACAACCTGATGATTGGCATCTTCATCTC	15 7530	8 8 8
7.2; DB 1; Length 110000; b. 9.2e-60; tches 443; Indels 6; Gaps	Score 277.2; Pred. No. 9.2e 0; Mismatches	21.8%; imilarity 55.9%; Conservative	Query Match Best Local Simila: Matches 569; Cor	\$ # P
Ν 9	End 210000 210000 210000 310000 510000 610000 6110000 11110000 11210000 11210000 11210000 11210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 1210000 13100000 13100000 13100000 13100000 13100000 13100000 13100000 13100000 13100000 13100000 13100000 13100000	Begin 100001 2000001 3000001 6000001 6000001 1000001 1100001 1	Fragment Name BX936398_01 BX936398_02 BX936398_03 BX936398_05 BX936398_06 BX936398_10 BX936398_10 BX936398_11 BX936398_11 BX936398_11 BX936398_12 BX936398_15 BX936398_15 BX936398_16 BX936398_26 BX936398_36 BX936398_46 BX936398_46 BX936398_46 BX936398_46 BX936398_46	
BX936398 Accession BX936398	s rocas	o 48 fragment	e split int	RESULT 15 BX936398 WPCOMMENT Sequence
TTTTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCGACTGGT 1032	ATATTATTC CGGTTATTC	TTTTCTTATGCATCAGGAGATATTATTC	975 TTTTCT" 10164 ATCCCA	ß 8
CATTCCTGCAGCCAGAAGAG	AGATTAAGT 	CTTCCTAGGACAACTCAAAGATTAAGTTGACTTCGCACTC	915 CTTCCT 	ß 8
GAGTAAGACGCATGGAAGGTACCCGAATCC 97	よびななかななな	マセンかつ という アンボンス		?

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TITICTIANGCATCAGGAGANATTAITCCCANGNITITGCTGGTGAAATGCTCGACTGGT 1032	S CTTCCTAGGAACACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAATCC 974	S GAAAATGCACTCGACAAGCTTGAAGCATTCAACTAGCTTCAATGGACCAGATTTTTATGGG 914 	S TGTGCTGGTATTTACAATGCACCTGTAGCCTTGTCAGTATATGCGAAGGTGTTTGAAAAG 854 	TTTTTCTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAAAGAGTGTTCTTGTGGA 794 	CTCAAAAGAGATCCACAGGGAGGCACTTGTGTCAGCTGTAACAAGTGGAAGTAAAAGA 734	TTGAACAGGAATTCTCTCTCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCCAGTC 674	TITGITGAATCITGCACTGAAGGATTIGTTGCAGCAACTGTCACCCCACAACATCITGTT 614	CAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTAAG 554	GAGGTIGACAIGTTIGAIAGAGAAAAGGIATICAITGAAACGGTTCIAAGACCGTTGGIG 494	CTACAAGAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGTTACTAATCCT 434	GGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTTACCAGTT 374	ATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCT 314	CCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTCCT 254	CCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTTTA 194	

Search completed: February 12, 2005, 03:51:13 Job time : 5683 secs

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| Cgn2 6 ptodata/1 pubpaa/USO7 NEW PUB.pep: *
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 189313,
Sequence 149491,
Sequence 48169, A
Sequence 50426, A
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57595, A
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959 52.9 347 15 US-10-282-122A-69927 Sequence 69927, A 952.5 52.6 344 15 US-10-282-122A-44700 Sequence 778404, A 952.5 52.6 344 15 US-10-282-122A-44700 Sequence 775878 52.6 344 15 US-10-282-122A-4760 Sequence 775878, A 943 52.0 354 15 US-10-282-122A-75878 Sequence 63114, A 934 51.5 348 15 US-10-282-122A-72752 Sequence 72752, A 1934 51.5 US-10-282-122A-72752 Sequence 72752, A 1935 15 US-10-282-122A-58744 Sequence 54267, A 1935 15 US-10-282-122A-58744 Sequence 55550, A 1935 15 US-10-282-122A-58744 Sequence 5923, Ap 15 US-10-282-122A-58744 Sequence 6923, Ap 15 US-10-282-122A-58916 Sequence 6924, Ap 15 US-10-424-599-14949 Sequence 6924, Ap 15 US-10-424-599-14949 Sequence 6924, Ap 15 US-10-424-599-150183 Sequence 25068, Ap 16 US-10-282-122A-5209 Sequence 25069, Ap 17 US-10-282-122A-52160 Sequence 6922, Ap 17 US-10-282-122A-52160 Sequence 6922, Ap 17 US-10-282-122A-52160 Sequence 52409, Ap 17 US-10-282-122A-52160 Sequence 52409, Ap 17 US-10-282-122A-52160 Sequence 52409, Ap 17 US-10-282-122A-52160 Sequence 52260, Ap 17 US-10-282-122A-52160 Sequence 52260, Ap 18 US-10-282-122A-52160 Sequence 52260, Ap 18 US-10-282-122A-5293 Sequence 52993, Ap 18 US-10-282-122A-5293 Sequence 52933, Ap 18 US-10-282-122A-5233 Sequence 52933, Ap 18 US-10-282-123A-5233 Sequence 52332, Ap 5250 Seque	45	44	43	42	41	40	39	8	37	36	3 5	ω 4	ω ω	32	ω	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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Sequence 69927 Sequence 69927 Sequence 69927 Sequence 4700 Sequence 78404 Sequence 7878 Sequence 75878 Sequence 75878 Sequence 75878 Sequence 63114 Sequence 6314-1-282-122A-5876 Sequence 58744 Sequence 58744 Sequence 58744 Sequence 58744 Sequence 58744 Sequence 58744 Sequence 6923 Sequence 6924 Sequence 6924 Sequence 58744 Sequence 58744 Sequence 6924 Sequence 6924 Sequence 6924 Sequence 6924 Sequence 6924 Sequence 58746 Sequence 58746 Sequence 58746 Sequence 58740 Sequence 58760	15	17	15										15	15	15	IJ	16	15	15	16	15	15	15	15	15	16	5	15	15	15	15	15
Sequence 69927, Sequence 78404, Sequence 63114, Sequence 63114, Sequence 54267, Sequence 54267, Sequence 54267, Sequence 54267, Sequence 54267, Sequence 6923, Sequence 6924, Sequence 6924, Sequence 6921, Sequence 6921, Sequence 52160, Sequence 51058, Seq	-10-424-599-15552	-10-472-928-2332	-10-282-122A-7090	-815-242-5884	0-282-122A-7238	0-369-493-5496	0-15	0-282-122A-5299	0-282-122A-5762	0-282-122A-5707	-815	0-282-122A-5216	-10-282-122A-6084	-10-282-122A-5240	-10-335-977-6922	-10-424-599-25018	-10-76	-10-424-599-14949	-10-282-122A-6891	-10-767-701-51620	-10-339	-10-33	-10-282-122A-5555	-10-282-122A-5874	-10-282-122A-5426	-10-767-701-33604	-10-282-122A-7275	-10-282-122A-6311	-10-282-122A-7587	-10-282-122A-4470	-10-282-122A-7840	-10-282-122A-699
	equence 15552	2332,	70902,	equence 5884, Ap	Sequence 72383,	equence 5496,	equence 14392,	equence 52993,	equence 57626,	equence 57073,	quence 10858,	equence 52160,	equence 60843,	equence 52409,	e 6922,	250183	37668,	149490,	68916,	51620,	6924,	6923,	55550,	e 58744,	e 54267,	e 33604,	equence 72752,	equence 63114,	equence 75878,	equence 44700,	equence 78404,	e 69927,

ALIGNMENTS

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Sequence 7, Application US/10451554

| Sequence 7, Application No. US20040111769A1
| GENERAL INFORMATION:
| APPLICANT: Rodolphe Arthur Kanhonou APPLICANT: Rodolphe Arthur Kanhonou APPLICANT: Rodolphe Arthur Falau |
| APPLICANT: Rodolphe Arthur Kanhonou |
| APPLICANTON USSAT Beet |
| FILE REFERENCE: 1187-24 |
| CURRENT APPLICATION NUMBER: US/10/451,554 |
| CURRENT FILING DATE: 2001-06-20 |
| PRIOR APPLICATION NUMBER: PCT/EP01/15093 |
| PRIOR APPLICATION NUMBER: EP 00870319.1 |
| PRIOR APPLICATION NUMBER: US 60/271,656 |
| PRIOR APPLICATION NUMBER: US 60/271,656 |
| PRIOR FILING DATE: 2001-02-26 |
| PRIOR FILING DATE: 2001-02-26 |
| PRIOR FILING DATE: 2001-02-26 |
| SOFTWARE: Patentin version 3.1 |
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                                                                                                                                                                                                                                                                                 ; LENGTH: 345
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-10-451-554-7
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61 SLPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCL
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Sequence

13

US-10-437-963-189313

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301 301

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APPLICANT: La Ross, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 189313
LENGTH: 359
Type: Dem
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 78.1%;
Conservative
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Publication No. US20040123343A1
                                                                                                242 RFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFY 301
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78.1%; Pred. No. 8.3e-140;
vative 39; Mismatches 36; Indels
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              US-10-282-122A-48169

Sequence 48169, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 199491, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5223)B
CURRENT APPLICATION WHERE: US/10/424,599
INUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
SEQ ID NOS: 285684
FEATURE:
PARTURE:
COCATION: (1)..(379)
OTHER INFORMATION: unsure at all Xaa locations
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_106012C.1.pep
US-10-424-599-149491
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US-10-424-599-149491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 80.2%; Score 1454; DB 15; Best Local Similarity 78.0%; Pred. No. 2.3e-139; Matches 269; Conservative 36; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                    YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDWLPAP 345
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Yamamoto, Robert
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ORGANISM: Oryza sativa

FEATURE:

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132

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RESULT 5
US-10-282-122A-50426
J Sequence 50426, Application US/10282122A
Publication No. US220040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 48169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGMTFEPLMTLYLTDNTPPDEIRRARESGFVHGVKLYPAGATTNSDHGVTDL-AKCAKT 140
                                                                                                                                                                                                                                                   YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
                                                                                                                                                                                                                     YGLPRSAETVTLRREPWELPREIFAGETPVVPLRGGETIGW 361
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Pred. No. 6.3e-100;
Mismatches 95;
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                             RESULT 6
US-10-282-122A-77674
; Sequence 77674, Ap
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

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PRIOR FILING DATE: 2000-09-06

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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 352
TYPE: PRT
ORGANISM: Burkholderia mallei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
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309
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                                                                               PRFFLGTDSAPHAKGAKEAACGCAGCYTALHALELYAEAFDQAGALDKLEGFASFFGADF
                                                                                                                                                                           FVE--SCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGS
                                                                                                                                                                                                                                     LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182
                                                                                                                                                                                                                                                                                                                                                      PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                                                                                                                                                                                                                                                                                                                                                      LTLARPDDWHLHVRDGAMLAAVLPHTARQFGRAIIMPNLKPPVTTTAQAQAYRBRILAAV
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|:::|||||||:|| | || || |:::
                                     YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
                                                                                                            KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDF 300
                                                                                                                                                          YVRDADAASGRIGATITAHHLLYNRNAMFFGGIRPHYYCLPVLKRETHRIALVEAATSGN
                                                                                                                                                                                                                                                                                                                       PAGMTFEPLMTLYLTDNTPADEIRRARESGCVHGVKLYPAGATTNSDAGVTDLLGKCAKT 128
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Wall, Da
YGLPRSAETVTLRRETWELPREIDAGAGPVVPLRGGEAIGW
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Yamamoto, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.4%; Score 1058; DB 15
58.4%; Pred. No. 5.6e-99;
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Application US/10282122A

Publication No.

US20040029129A1

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Remaining Prior Application data removed - Set NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 77674
LENGTH: 350
TYPE: PRT
ORGANISM: VUbrio cholerae
US-10-282-122A-77674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 200;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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PRIOR ETLING DATE: 2000-12-22
PRIOR PILLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
303 LERNNSKIKLSKTEWKVPESFSYASGDIIEMFAGEMLDW 341
                             249 ÉFLGTDSAÞHAKGRKÉAACGCÁGSYTÁHAÁLELÝÁBVFBKEGKLENLEÁFASÍNGÞDFYG
                                               243 FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDPYG 302
                                                                                        183 FVESCTEGFVAATVTPQ0HLVLNRNSLFQGGLQPHNYCLFVLKREIHREALVSAVTSGSKR 242
                                                                                                                       130 LÓAMQÉVGMLLÍVHGEVÍTHEVDIFDRÉKTFLDTVLAÞÍVNDFÞQLKIVLEHITTAÐÁVT 189
                                                                                                                                          123 LQEMVEHNMPLLVHGEVTNÞEVDMFDREKVFIETVLRPLVQKFFQLKVVMBHVTTIDAVK 182
                                                                                                                                                                                     63 PVDSDENPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                                                                                                                                                                 FVQQAGDN-VAÀTITAHHLLFNŘNHMLVĠĠIRÞHFÝĆLÞILKŘATHQHALVAÀATŠĠŠKK 248
                                                                                                                                                                    P-QAHÉEBĹMALYLTDNÍSÞEBÍRKÁKASGKVVAAKLÝÞÁGÁTTNSDSGVÍSA-KNIYÞV 129
                                                                                                                                                                                                                                                                                       Conservative
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Forsyth, R.
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Malone, Cheryl
Haselbeck, Robert
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Vamamoto, Robert
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Trawick, John
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Zyskind, Jud
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dio, Carlos
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CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,636

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-26

PRIOR PILING DATE: 2001-02-26

PRIOR PILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16
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US-10-282-122A-51386
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sim
Matches 196;
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SEQ ID NO 51386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-282-122A-51386
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APPLICANT:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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188 REGAHYÚRD-AEGPTÁÁTITÞÓHMLYNRNAIFTGGVRÞHWÝCLÞILKREVHROÁLÍVEÁAT
                             178 IDAVKFVESCTEGFVAATVTPOHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVT 237
                                                                                                                       128
                                                                                                                                                           118
                                                                                                                                                68 ĹRKAGGĎTAAFTÞĹMTĹÝĹŤĎNŤPAEBÍVRÁHĖŚGQVAAVKLÍÝPÁGÁŤTNŠDAĞVŤĎĹLĠ 127
                                                                                                                                                                                  59 LKSLPVD-SDENPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFG 117
                                                                                                                                                                                                                                                  KCLPVLQEMVEHNMPLLVHGSVINPEVDMFDREKVFISTVLRPLVQKFPQLKVVMEHVTT 177
                                                                            KĊGAAĹAALERCGMPĹĹVĤĠĖVŤDPAſĎVFĎŘĖĄVĖÍĖRVMQPĹRRAYPGĹKVVFĖĤſŤŤ
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Forsyth, R.
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Trawick, John
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Zyskind, Judith
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Grant
To, Robert
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6.3e-94;
hes 97; Indels
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US-10-282-122A-65811
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PRIOR PILLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
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PRIOR PILLING DATE: 2000-09-06
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PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-11-27
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LENGTH: 344
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                       123
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192; Conserv
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LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182
                                                                                                                                                                                        LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL 62
                                                                PEGSAFEPLMTLYLTDQATPALVREAKAAGIV-AFKLYPAGATTNSDSGVTDLF-KLIPV
                                                                                                      PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                                                                                                                LTIIR POOMHLHLROGDALKAVAPYTARQMGRAVIMPNIKPPVVSVADALAYKARIMAAL
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Zyskind, Judith
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Malone, Cheryl
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US-10-282-122A-65238
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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                                                                                           Query Match
Best Local
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                   TYPE: PRT ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                        LENGTH: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSK-
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                                                                                               Similarity
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Zyskind, Judith Wall, Daniel
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Malone, Cheryl
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                                                                       54.0%; Score 979; DB 15; ilarity 56.3%; Pred. No. 6.2e-91; Conservative 55; Mismatches 88
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APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
APPLICANT: Williamoto, Robert
APPLICANT: Williamoto, Robert
APPLICANT: Misser Holliamoto, Robert
APPLICANT: Misser Hol
                                                                              Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 59728
LENGTH: 348
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59728
             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-10-282-122A-59728
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                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59728, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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             55.8%;
Score 978; DB 15;
Pred. No. 8e-91;
                           Length
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AFFLICANT. Xu, H.

APPLICANT: Xu, H.

FILE REFERENCE: ELITRA, 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION AUMBER: 60/269,308

PRIOR APPLICATION AUMBER: 60/269,308

PRIOR APPLICATION AUMBER: 60/269,308
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US-10-282-122A-66489
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Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66489
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carl
APPLICANT: Malone, Chery
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Publication No. US20040029129A1
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Zyskind, Judith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto,
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Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trawick, John
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; TYPE: PRT; ORGANISM: Pseudomonas US-10-282-122A-66489
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        FILE REPERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT EILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR APPLICATION NUMBER: 60/267,636
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US-10-282-122A-43220
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Rob
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judit
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43220, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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Zyskind, Judith
Wall, Daniel
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Malone, Cheryl
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Yamamoto, Robert
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NUMBER: 60/269,308
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Pred. No. 1.6e-90;
3; Mismatches 106;
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                                                   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms;
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43220
LENGTH: 348
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robe:
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Publication No. US20040029129A1
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hes 189;
                  APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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Carr, Grant
Carr, Grant
Carr, Grant
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Forsyth, R.
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Trawick, John
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ilarity 55.8%;
Conservative 46
      NUMBER:
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; Pred. No. 4.2e-90;
46; Mismatches 102;
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RESULT 14
US-10-282-122A-69927
, Sequence 69927, Application US/10282122A
, Publication No. US20040029129A1
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          APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-29
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOPTWARE: Patentin version 3.1
SEQ ID NO 67595
                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
APPLICATION NUMBER: 60/230,335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR 242
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                                                                                                                                                                                                  Yamamoto, Ro
Forsyth, R.
                                                                                                                                                                                                                                                    Wall, Daniel
Trawick, John
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Zyskind, Judith
Wall, Daniel
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Pred. No. 3.
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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US-10-282-122A-78404
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US-10-282-122A-69927
                                                                                                                                                                                                                                                                                                                                                                       Sequence 78404, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PRIOR DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PRIOR PRIOR DATE: 2010-12-26
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
APPLICANT: Forsyth, R.
APPLICANT: You, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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Best Local Similarity
Matches 187; Conserv
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 69927
LENGTH: 347
TYPE: PRT
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                                                                                                                                          Carr, Grant
Carr, Robert
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; TYPE: PRT
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US-10-282-122A-78404
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PRIOR APPLICATION NUMBER: 60/206,848

PRIOR TILING DATE: 2000-05-23

PRIOR PELLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-05-26

PRIOR PILLING DATE: 2000-09-06

PRIOR PILLING DATE: 2000-09-06

PRIOR PILLING DATE: 2000-09-09

PRIOR PILLING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILLING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILLING DATE: 2000-11-23

PRIOR PILLING DATE: 2000-11-23

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILLING DATE: 2000-12-22

PRIOR PILLING DATE: 2001-12-29

PRIOR PILLING DATE: 2001-02-09

PRIOR PILLING DATE: 2001-02-16

PRIOR PILLING DATE: 2001-02-16

PRIOR PILLING DATE: 2001-02-16

PRIOR PILLING DATE: 2001-02-16

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PRIOR PILLING DATE: 2001-02-16

PRIOR PILLING DATE: 2001-02-16
Search completed: February 12, Job time : 82 secs
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 78404
LENGTH: 348
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Best Local Similarity 53.4%;
Matches 181; Conservative 5
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Pred. No. 1.4e-88;
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-252-991A-17491
US-09-252-991A-18106
US-09-248-796A-18106
US-09-248-796A-18106
US-09-248-796A-18106
US-09-107-532A-5107
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Sequence 7589, Ap
Sequence 17491, A
Sequence 5541, Ap
Sequence 2330, Ap
Sequence 18106, A
Sequence 11399, A
Sequence 5107, Ap
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Sequence 3844, Ap
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Sequence 126, App
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Sequence 69, Appl
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Sequence 18889, A
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RESULT 2

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RNNSKIK :: VNESYVE	വ—വ ഗ	RMVEHNM:	VDSDFNPLI AGHDFTPLI	TQPDDWI : RRPDDWI	milarity Conserva	9A-7589 589, Applica 6610836 6610836 FORMATION: Gary Bret INVENTION: INVENTION: INVENTION: FILICATION NUM ILING DATE: LICATION NUM ILING DATE: LIC		4444444444444444444
LSKTPWK : LVREETT	VAATVTP:: : : : LAATITP: HDRRRKE: HARHRKE	PLLVHGE 	WICXTID	HLHLRDGI : HIHLRDDI	54.0 55.8 tive	ation US/09. ton et. al NUCLEIC AC PNEUMONIA 9.2004001 NUMBER: US/ 2000-01-2 9: 14342 a pneumonia		7344433 22444434 2244443 2244443 2244443 2244443 2244443 22444433
LPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341 	FVESCTEGFVAATVTPOHLVLNRNSLFOGGLOPHNYCLPVLKREIHREALVSAVTSGSKR FVESCTEGFVAATVTPOHLVLNRNSLFOGGLOPHNYCLPVLKREIHREALVSAVTSGSKR YVRDGNE-LLAATITPOHLMINIMLVGGIRPHLYCLPVLKRNIHOQALRELVASGFSR YVRDGNE-LLAATITPOHLMINIMLVGGIRPHLYCLPVLKRNIHOQALRELVASGFSR FFLGTDSAPHDRRRKEGCGAGGRINHMLVGGIRPHLYCLPVLKRNIHOQALRELVASGFSR FFLGTDSAPHDRRRKEASCGCAGCFNAPTALGSYATVFEEMNALQHFEAFCSLNGPRFYG AFLGTDSAPHARHRKEASCGCAGCFNAPTALGSYATVFEEMNALQHFEAFCSLNGPRFYG	LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK - - - - - - - - - - - - -	pvdsdenplmtlyltdttspmeiklaresqyvfgyklypagattnsqdgytdlegkclpv 	LSITOPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL 	%; Score 978; DB 4; Length %; Pred. No. 1.8e-98; 46; Mismatches 102; Inde	89039A D AND AMINO ACID SEC FOR DIAGNOSTICS AND 99/489,039A 9/117,747	ALIGNMENTS	US-09-809-665A-117 US-08-469-318-127 US-08-468-609A-127 US-08-446-872A-127 US-08-4762-227A-127 US-08-762-227A-127 US-08-875-533-70 US-09-497-585A-8 US-09-497-585A-8 US-09-360-501A-14 US-09-360-501A-14 US-09-360-545-32 US-09-360-545-32 US-09-360-545-32 US-09-360-545-32 US-09-360-545-32 US-09-360-545-32 US-09-360-545-32 US-09-360-545-32 US-08-468-0318-136 US-08-468-0318-136 US-08-468-0318-136 US-08-468-72A-136 US-08-468-72A-136 US-08-762-227A-136
w -	NIHCALVSAVTSGSKR 242	19	TINSQDGVTDLFGKCLPV 122	TTTAAAVAYREAILKSL 62 : : : :: TTVAAAIAYRQRIMDAV 71	ngth 352; Indels 2; Gaps 2;	UENCES RELATING TO KLEBS!		Sequence 117, App Sequence 127, App Sequence 127, App Sequence 127, App Sequence 127, App Sequence 127, App Sequence 127, App Sequence 70, Appl Sequence 14, Appl Sequence 14, Appl Sequence 2593, Ap Sequence 137, Appl Sequence 137, Appl Sequence 137, Appl Sequence 136, Appl Seque

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                                                                                                                      ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5541
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US-09-328-352-5541
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                                                                                                                                                                    Sequence 5541, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
RUMBER OF SEQ ID NOS: 8252
ENGTH: 346
TYDE: 1939-06-04
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17491
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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     3 LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL
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                                                    Conservative
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                                            52.6%; Score 952.5; DB 4; 53.8%; Pred. No. 1.1e-95; tive 57; Mismatches 97;
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55.5%; Pred. No. 4.7e-98;
tive 43; Mismatches 106;
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RESULT 5
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Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
LENGTH: 355
TYDED: DEED
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                                                                                                                                                                                                                                      66 K-DSDLPATRKDSFDPRMVLYLTDOTTAKDIDDAAQTGIVSAVKLYPAGATTNSADGVTD
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AŚRYGAQFYGLAINTTQITLIKOPOTIPESFHYLGNKTLTPLLAGEVLPW
                           TSFNGPDFYGLPRNNSKIKLSKTPWKVPESFSY-ASGDIIPMFAGENLDW 341
                                                         LEVATSGNPKFFLGTDSAPHATHTKESSCGCAGCYSALHALPLYAMAFESVNALDKLENF
                                                                            VSAVTSGSKRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAF 292
                                                                                                                                       VTTIDAVKFVESCTE--GFVAATVTFQHLVLNRNSLFQGGLQPHNYCLFVLKREIHREAL
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53.4%; Pred. No. 5.9e-95;
tive 50; Mismatches 97;
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US-09-248-796A-18106
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                                                                                             ; ORGANISM: Candida albicans US-09-248-796A-18106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4285
LENGTH: 356
TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR PRILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18106

LENGTH: 365

TYPE: DET
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Patent No. 6605709
GENERAL INFORMATION:
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            Query Match
Best Local Similarity
Matches 139; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVLEGNE-FLGATITPQHLMFNRNHMLVGGVKPHLYCLPILKRNVHQEALRQAVASGHSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSGDKEEPLMTCYLTDSTLPSEVEQGFLQGVFTACKLYPANATTN8SHGVSDI-NKIYPI 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFLGTDSAPHLQHRKESSCGCAGVFNAPTALAAYASVFKELNALSHFEAFCSLNGPRFYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
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              28.8%; Score 522.5; DB 4 llarity 38.3%; Pred. No. 1.6e-48; Conservative 57; Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.3%; Score 930; DB 4; 52.8%; Pred. No. 3.4e-93;
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                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107;
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                                                     Length 365;
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                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
FITLE OF INVENTION: Myxococcus xanthus Genome Section of the Current Application NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11399
LENGTH: 734
TYPE: PRT
ORGANISM: Myxococcus xanthus
ORGANISM: Myxococcus xanthus
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 ALDKLEAFTSFNGPDFYGL-----PRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 EIHREALVSAVTSGSKRFFLGTDSAPHDRRRKECSCG-CAGIYNAPVALSVYAKVFEKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 EHCTTSDAVETVRELNSNYKPGDELFVGATITAHHLYLIIDN-WAG--NPINFCKPVAKF
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                      193
                                                                                                                                                                                                                                                                                                                                     10 DWHLHLRD-GD-----VLKAVVSHSAHHFGRAIVMENLKPPITTTAAAVAYREAILKSLP
                                                                                                                                                                                                                                                           64 VDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDG------
                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKCLPVLQEMVEHNMPLLVHGE----VTNPEVDMEDREKVFIETVLRPLVQKFPQLKVVM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKLAP-QTTF--LMSFYLSKDLTP---ELIEECADLIHGVKCYPAGVTTNSKYGVDPNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IELGITA--DMHVHLRDGSMCE-LITPTVRTGGIAISYVMPNLVPPITTKQQVVNYHTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAI--VMPNLKPPITTTAAAVAYREAI
                                                                                                                                                                                                                                                                                                    DLHVHLREPGEEGKETVLTGCRAAVÄGGFTAVVAMPNTK----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHVTTIDAVKFVESCT-----EGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKR
                                                            LRGIPASAEVAMVARDIVLLEET-----KGRLHVAHVSCEGSVRLIREAKRSGLRV
AATVTPOHLVLNRNSLFOGGLQPHNYCLFVLKREIHRBALVSAVTSGSKRFFLGTDSAPH
                                                                                                                                      GCVAITD-DGR--PVMNASLMRRTLQYATQFDVPVMVHEEDLTLSAGGAMHEGTTSTRLG
                                                                                                                                                                                ----VTDLFGKCLPV------LQEMVEHNMPLLVH-----
                                                                                             -GEVINPEYDMFDREKYFIETVLRPLVQKFPQLKVVMEHVITIDAVKFV-ESCTEGF-V
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                                                                                                                                                                                                                     -----VVNDNAMVTELVLNR-ARAAGLCHVYPAGAITKGLKGEELAEMGELVSA 445
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                                                                                                                                                                                             Matches
                                                                                                                                                                                                             Query Match
Best Local :
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US-09-107-532A-5107
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-UIII-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
165 TMYLAMKÉAAKNNKALVAH---TEDÉSLLÉGGVMHAGKKAÉELGLÉGTÍSVTESSQIARD 221
                             118 KCLPVLQEMVEHNMPLLVHGEVTNPEVDMF-----DREKVFIETVLRP----
                                                                          122 VKVLQY----
                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: YE ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-01 TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007 TELEFAX: (781)893-8277
                                                                                    59 LKSLPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYFAGATTNSQDGV-TDLFG
                                                                                                                                          10 DWHLHLRD-GDVLKAVV-----SHSAHHFGRAIVMPNLKP-PITTTAAAVAY----REAI
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
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                                                                                                                                                                                            l Similarity 67; Conserv
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                                                                                                                 DVHVHĽKEPGFTYKETIEAGTRŚAARGGFTTVCANPNINPVPDTAEKLRQVYDIIRKDAV
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 430 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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STATE: Massachusetts
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                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                YES
                                                                                                                                                                                                  6.6%;
                                                                                                                                                                            Score 119.5; DB 4;
Pred. No. 0.00031;
3; Mismatches 114;
                                                         -APITENL-RSEKLVDQEALIEEGAFAFTNDGVGVQTAG
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                     Length 430;
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                                                                                                                                                                         Gaps
                             160
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US-09-583-110-3844
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                                                                                                                   Sequence 3844, Application US/09583110 Patent No. 6699703
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Best Local Similarity
Matches 80; Conserv
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SEQ ID NO 6087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
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GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus;

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATHO0-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACI

ITILE OF INVENTION: ENTERCOCCCUS FAECALIS FOR

FILE REFERENCE: 032796-032

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US/09/134,000C

PRIOR FILING DATE: 1997-08-15

PRIOR FILING DATE: 1997-08-15

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                   344 FGIVGSETAFQLIYTNFVETGIFTLEQVID 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 SQIARDITLAKETGVHYHVCHVSTEESVRVIRDAKKAGIHVTÄBVSPHHLILVDEDIPGD 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 KCLPVLQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQK---FPQLKVVME- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 VKVLQYAPITEELRSEVLTNQKA---LKEAR------ÀFAFTŃ--DĠVGVQTAĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 DWHLHLRD-GDVLKAVV---SHSAHHPGRAIV--MPNLKP-PITTTAAAVAY----REAI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 - LVQKFPQLKVVMEHYTTIDAVKFVESCTEG--FVAATVTPQHLVLNRNSLFQGGLQPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAL------SVYAKVFEKENALD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGFWKMY---PPLRGLADRQÁLIDGLLDGTID-CIATDHÁPHGLEEKQQŚ-----FLNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGLQPHNYCLPVLKREIHREALVSAVTSGSKRFFLGTDSAPHDRRRKECSCGCAGIYNAP 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMYLAMKÉAAALMMAĹVAHTÉ-----DESLLFGGVMHEGEVSKKLGLFGILSATEA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKSLPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVPGVKLYPAGATTNSODGV-TDLFG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVHVHFREPGFTYKETIKTGSKAAARGGFTTVCAMPNLNPVPDTAEKLSEVYDLIQKDAV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCL----PVLKREIHREALVSAVTSGSKRFFLGTDSAPHDRRRKECS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGFWKMNPPLRGREDREALIEGLLDGTID-CIATDHAPHGLEEKSQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09134000C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.4%; Score 116.5; DB 4;
24.2%; Pred. No. 0.00069;
ative 39; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------HVTTIDAVKFVESCTEG--FVAATVTPOHLVL-NRNSLFQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACID SEQUENCES RELATING
FOR DIAGNOSTICS AND THEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321
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; PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 1998-05-12; PRIOR FILING DATE: 1997-07-02; NUMBER OF SEQ ID NOS: 5322; SEQ ID NO 3844; LENGTH: 422
                                                                                                                                                                                                                                                                                                                                                                                                  3-09-107-43, Application:
Sequence 3349, Application:
Sequence 300744
Patent NO. 6800744
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-107-433-3349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                              APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                    ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamel
                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVKTVATITKNEN---GKNLTDEKALLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGMTGLETSLSLGLTYLVEAGELSLMELLEKMT-YNPAKLY 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTQGSNAKMN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LF-QGGLQPHNYCLPVLKREIHREALVSAVTSGSKRFFLGTDSAPH---DRRRKECSCGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEYAMMARDVMIAYATKAHVHIQHLSKEESVKVVE-FAQGLGAEVTAEVAPQHFSKTEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SK---IVKEAMEEAKKL-----NTFISLHEEDPGLNGVLGFNENIAREHFHICGATGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKCLPVLQEMVEHNMPLLVHGEVTNPEVDMFDREK-----VFIETVLRP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIHVHFREPGQTHKEDIHTGALAAAAGGFTTVVWMANTSPTISDVETLQAVLQSAAKEKI 116
                                                                                                                                                                                                           COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGIYNAPVALSV---YAKVFEKENALDKLEAFTSFNGPDFY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------LVQKFPQLKVVMEHVTTIDAVKFVESCTEGF---VAATVTPQHLVLNRNS
                                                    APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                     MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                              02354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PPLRLESDRRAVIEGLKSGVIT-VIATDHAPHHVDEKNVEDITKAP 321
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Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AGAVGFSDDGIPLES 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
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                                                        ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-09-710-279-628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-710-279-628
                                                                                                                                                   APPLICANT: KIMMERIX, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOUTWARE: Patentin Ver. 2.1
SEQ ID NO 628
LENGTH: 371
TYDE: PRT
                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6703492
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 628, Appl
Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMOUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3349:
SEQUENCE CHARACTERISTICS:
                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 GKCLPVLQEMVEHNMPLLVHGEVTNPEVDMFDREK-----VFIETVLRP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DIHVHFREPGQTHKEDIHTGALAAAAGGFTTVVWMANTSPTISDVETLQAVLQSAAKEKI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 DWHLHLRD-----GDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGIYNAPVALSV---YAKVFEKENALDKLEAFTSFNGPDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LF-QGGLQPHNYCLPVLKREIHREALVSAVTSGSKRFFLGTDSAPH----DRRRKECSCGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEYAMMARDVMIAYATKAHVHIQHLSKEESVKVVE-FAQGLGAEVTAEVAPQHFSKTEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LVQKFPQLKVVMEHVTTIDAVKFVESCTEGF---VAATVTPQHLVLNRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SK---IVKEAMEEAKKL-----NTFISLHEEDPGLNGVLGFNENIAREHFHICGATGV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 426 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGMTGLETSLSLGLTYLVEAGELSLMELLEKMT-YNPAKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLTQGSNAKMN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09710279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLRLESDRRAVIEGLKSGVIT-VIATDHAPHHVDEKNVEDITKAP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 103.5; DB 4; Pred. No. 0.017;
      Score 102.5; DB Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae
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269

160

Length

131;

85;

Gaps

16

61

Length 426; Indels

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GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PUJ480US

CURRENT APPLICATION NUMBER: US/09/710,279

PRIOR FILING DATE: 2000-11-09

PRIOR REPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09

SOFTWARE: Patentin Ver. 2.1

SEO ID NO 2604

LENGTH: 425

TYPE: PRT

ORGANISM: Artificial Sequence
RESULT 14
US-09-134-001C-4803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
US-09-710-279-2604
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Best Local (
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RESULT 15
US-08-469-318-126
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ITITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
ITITLE OF INVENTION: REPIDERMIDIS FOR DIAGNOST
FILLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PHILING DATE: 1997-11-08
PRIOR PHILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 427
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                                                                                         FILING DATE:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6022
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Best Local Similarity
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TITLE OF INVENTION: Prot
NUMBER OF SEQUENCES: 190
COMPUTER READABLE FORM:
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                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
    MOLECULE TYPE:
                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,318
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                    STRANDEDNESS:
TOPOLOGY: 1:
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OPERATING SYSTEM:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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protein
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 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1067.5
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Maximum Match 100
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Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqp2000s:*
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2005, 05:12:50 ; Search time 92 Seconds (without alignments)
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Abu38565
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Adf04000 Bacteria: Abu26343 Protein Abu30820 Protein Abu30820 Protein Abu27626 Protein Abu27626 Protein Abu40992 Protein Abu40992 Protein Abu40992 Protein Abu40993 Protein Abp06300 Human OR Abp06300 Human OR Abu24485 Protein Abu24495 Protein Abu47703 Listeria Abu32919 Protein Abu47121 Thermoco Adb11184 Alloioco Adb11184 Alloioco Adu35265 Enteroco Abu59149 Protein Abu54385 Lactococ Abu29149 Protein Abu54385 Lactococ Abu29702 Protein Abu59300 E. faeci	
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RESULT 1 AAB707 XX AAB77 XX AAB77 XX AAB77 XX POta XX Pota XX AAB70773 standard; protein; 01-MAR-2001. WO200114569-A2 Solanum tuberosum uridine; starch synthesis Potato; dihydro-orotase; plant; polysaccharide content; orotic acid; Potato dihydro-orotase protein 25-MAY-2001 (first entry) AAB70773; 346 ₽

12-AUG-2000; 2000WO-EP007884 20-AUG-1999; 99DE-01039688

Ehrhardt T, Schroeder M; Stitt Nigel Σ, Geigenberger PL, Loef H Zrenner

æ

WPI; 2001-202938/20. N-PSDB; AAF61217.

(BADI) BASF

Increasing the polysaccharide, especially starch, content of plants, transforming with a sequence encoding dihydro-orotase. γď

Example 4; Page 30-31; 32pp; German.

This invention describes a novel use of a DNA sequence (I) encoding dihydro-orotase (II) to prepare plants which have increased polysaccharide (PS) content. The invention also describes (1) a 1271 base polysaccharide (PS) content. The invention also describes (1) a 1271 base polysaccharide (PS) content. The invention also describes (1) a 1271 base it and its homologs (or their fragments); (2) method for preparing plants of increased PS content by expressing (II) in them; (3) method for transforming plants by introducing an expression cassette, containing promoter, signal sequence and (I), into a plant cell, callus tissue, complete plant or protoplast; and (4) plants with increased PS content containing the DNA of (I). Expression of (II) increases the content of orotic acid (a precursor of uridine nucleotides), resulting in an increased rate of starch synthesis. Typically, in potato tuber slices,

Protein

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RESULT 2
AAB70779
ID AAB7
XX AAB7
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Matches 346
This invention describes a novel DNA sequence (I) containing the coding region for a plant dihydro-orotase (DHO), comprising a sequence (S1) of
                                                                                     Claim 3; Page 31-32;
                                                                                                                      New DNA encoding plant dihydroorotase, plants and for screening for compounds and that be used as herbicides.
                                                                                                                                                                                                                                                                                       Ehrhardt T,
                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    02-SEP-2000; 2000WO-EP008581
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                                                                                                                                                                                                                                                                                                                                      (BADI )
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                                                                                                                                                                                                                                                                              Sugar beet; transgenic plant; osmotic stress tolerance; oxidative stress tolerance; casein kinase alpha catalytic subunit; dihydroorotase; translation initiation factor 1A; plant flowering; plant growth stimulation.
                                                                                                                                                                  WO200252012-A2
                                                                                                                                                                                                                                               Beta vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta vulgaris dihydroorotase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO15493 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vkfvesctegfvaatvipohlvlininslfogglophnyclfvlkkeihrealvsavisgs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLPVDSDFNPLMTLYLTDTTSPMEIKLÁRESÓVVFGVKLYPÁGÁTTNSÓÐGVTÐLFGKCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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20-DEC-2001; 2001WO-EP015093

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RESULT 4
ABUZ0245
ID ABUZ
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AC ABUZ
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Best Local S
Matches 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of sugar beet (Beta vulgaris) genes that are involved in osmotic and oxidative stress tolerance in a plant. The Beta vulgaris genes of the invention encode the proteins: casein kinase alpha catalytic subunit; dihydroorotase; translation initiation factor 1A; putative protein; and an unknown protein. The Beta vulgaris genes of the invention are useful for enhancing the osmotic and oxidative stress tolerance of a plant. The Beta vulgaris genes are also useful for stimulating plant growth. The casein kinase alpha catalytic subunit gene is useful for controlling the process of flowering in a plant. The present amino acid sequence represents the Beta vulgaris dihydroorotase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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26-FEB-2001; 2001US-0271656P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CROP-) CROPDESIGN
                                            Antisense; prokaryotic
                                                                           Protein encoded by
                                                                                                                                                                      ABU20245
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|||::|:||||||||||::|:
MELTLTRPDDWHLHLRDGDLLAAVAPHSARHFGRAIVMPNLRPPVTTTGAAIAYRKSIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLPDDSDFNPLMTLYLTDTTSPNEIKLARKSEVVYAVKLYPAGATTNSQDGVTDLLGKCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCL 120
                                                                                                                                                                                                                                                                           YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDWLPA 344
                                                                                                                                                                                                                                                                                                                               KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDF 300
                                                                                                                                                                                                                                                                                                                                                                                             VKFVESCTEGFVAATVTPOHLVLNRNSLFQGGLQPHNYCLFVLKREIHREALVSAVTSGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLEEMAEQDMPLLVHGEVTDPDVDIFDREKVFIESVLRPLIQKLPQLKVVMEHITTADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVLQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDA 180
                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                   YGLPRNTSKIKLKKEPWKVLERIPFPSGEIIPMFAGQMLDWKPS
                                                                                                                                                                                                                                                                                                               KQYFLGTDSAPHERRRKECSCGCAGIYNSPVALSLYAKVFEEAGALDKLEAFTSFNGPDF
                                                                                                                                                                                                                                                                                                                                                                           VKFIESCNGGNVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHRQALVSAVTSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                           (first entry)
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                                                                           Prokaryotic
                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.3%;
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                                             essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1528; DB 5;
Pred. No. 6.9e-145;
4; Mismatches 28;
                                                                                                                                                                         364
                                                                            essential gene
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Best Loc Matches

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Similarity

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1.9e-98;

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LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182 PAGMTFEPLMTLYLTDNTPPDEIRRARESGFVHGVKLYPAGATTNSDHGVTDL-AKCAKT PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122

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ct the 5213 antisense sequences given in the specification where expression confirmation of a cell. Also included are:

((1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (4) an antibody capable of specifically binding compound that inhibited by the containing the vector; (4) an isolated containing the vector; (4) an isolated for containing the vector; (4) profileration of an organism acts; (4) an antibody capable of a prodiferation of an isolated product it is overexpressed or underexpressed; (12) determining the extent containing the activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent containing the vector of a compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent containing the vector of a containing the vector of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational contained for cellular proliferation to isolate candidate molecules for rational contained for cellular proliferation in cells other than S. aureus, S. typhimurium, C. patent did not form part of the printed specification, but was obtained in electronic format directl
                                   Query Match
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Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 48169; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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                                                                          Sequence 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Δħ
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)B; ACA24115.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELITRA
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Carr G
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                  58.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for rational drug
Score 1067.5;
Pred. No. 1.9e
97; Mismatches
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                                         DB 6;
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Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery
                                       Length
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Xu HH;
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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC nucleic acid; (4) an antibody capable of specifically binding CC polypeptide or its fragment whose expression is inhibited by the antisense cc polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for crequired for proliferation, (7) identifying a compound that influences the activity of identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an activity against a biological pathway in which a proliferation-required gene or its gene product lies or pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which a proliferation or
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                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 50426; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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06-SEP-2001; 2001US-00948993.

25-0CT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-0362699P.
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Trawick JD,
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Yamamoto R,
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                          21-MAR-2002; 2002WO-US009107.
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                                                                                                                                                                                                                                                                                                                                        ABU49750 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for for cellular proliferation to isolate candidate molecules for rational required drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, the target prokaryotic essential genes. Note: The sequence data for this in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 352 AA;
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Pred. No. 1.7e-97;
5; Mismatches 95
                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                 gene; cell proliferation; drug design.
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(ELIT-)

ELITRA PHARM

INC

Wang Wall

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Zamudio Trawick

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Malone Carr (, 6, 9,

Haselbeck R, Yamamoto R,

Claim 25; SEQ ID NO 77674; 1766pp; English isolate candidate molecules for rational drug

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Co polypeptide or its fragment whose expression is inhibited by the control or its fragment whose expression is inhibited by the collisers nucleic acid; (4) an antibody capable of specifically binding control or the polypeptide; (6) inhibited by the collisers or the polypeptide; (6) inhibited by the polypeptide; (6) inhibited by the collisers or the polypeptide; (6) inhibiting cellular collisers or proliferation or the activity of a gene in an operon required for collisers or required for proliferation, or that inhibite goalmant a biological pathway or the proliferation, or that inhibite pathway of identifying a gene required for cellular proliferation or the biological pathway in which hat proliferation, or that inhibite gene product lies or agene on which the test compound that inhibite proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound acts in the proliferation of an organism acts; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibite proliferation of grains; or (13) identifying the target of a compound that inhibits the gene collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational content of the target prokaryotic essential genes. Note: The sequence is encoded by one of the target prokaryotic essential sense. Note: The sequence data for this content did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained content of the printed specification of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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the nucleic acid inhibits proliferation of a cell. Also included
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182
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                                                                                                                                                          FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
                                                                                                                                                                                                                                                                      FVQQAGDN-VAATITAHHLLFNRNHMLVGGIRPHFYCLPILKRATHQHALVAAATSGSKK
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Xu HH;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression (1) a vector comprising a promoter operably linked to the nucleic acid inhibits proliferation of a cell. Also included are: (2) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated concoding the polypeptide; (6) inhibited by the concoding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for concliferation, (7) identifying a compound that influences the activity of identifying a proliferation, or that inhibite cellular proliferation or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies compound that inhibits proliferation of an operon required for organism acts; (9) manufacturing an antibiotic; (10) profiling a compound acts; (9) manufacturing an antibiotic; (10) profiling a compound acts; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an occasion of an organism. The antibiotic; (10) profiling the extent to which each of the strains is present in a culture or collection of contiferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational contiferation and contiferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, contiferation in cells other than S. aureus, S. typhimurium, contiferation in cells other than S. aureus, S. typhimurium, contiferation in cells other than S. aureus, S. typhimurium, contiferation in cells other than S. aureus, S. typhimurium, contiferation in cells other than S. aureus, S. typhimurium, contiferation in cells other than S. aureus, S. typhimurium, c
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Forsyth
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Zyskind JW; Xu HH;

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123

63 72

12 w

190 183 Query Match Best Local Similarity

57.4%;

Score 1039.5; DB 6; Pred. No. 1.2e-95; Mismatches

200;

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45;

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Best Local Similarity 57.0
Matches 196; Conservative
Claim 25; SEQ ID NO 65811; 1766pp; English
                                                                                                                                                                                                                      Wang L,
Wall D,
                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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06-SEP-2001; 2001US-0094893.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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Carr GJ,
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57.0%; Pred. No. 1.6e-92;
tive 46; Mismatches 97;
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Forsyth
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RESULT 9
ABP78043
ID ABP7
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AC ABP7
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AC ABP7
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DT 07-M
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DE N. 9
XX

ABP78043 standard; protein;

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ABP78043; 07-MAR-2003

(first

entry)

N. gonorrhoeae amino acid sequence SEQ ID 2616

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of CC of the 6213 antisense sequences given in the specification where expression CC (1) a vector comprising a promoter operably linked to the nucleic acid compositing a promoter operably linked to the nucleic acid compositing a promoter operably linked to the nucleic acid compositing a polypeptide whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits ellular proliferation; (8) compound gene product or that has an activity against a biological pathway contained for proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for the strains; or (13) identifying the target of a compound that inhibits the gene of identifying proteins or screening for homologous nucleic acids required for proliferation in calls other than 8. aureus, 8. typhimurium, 100 contained to proliferation in calls other than 8. aureus, 8. typhimurium, 100 contained to proliferation in calls other than 8. aureus, 8. typhimurium, 100 contained to the proliferation of the printed specification, but was obtained the full for format directly from MIPO at the sequence data for this in electronic format directly from MIPO at the sequence at the sequence and the sequence and the sequence and the sequence and the sequence and the sequ
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                                                                            HKFFLGTDŚĄPHAKSAKĖNAČĠĆĄGMFSĄMTĄ IELYĄEVPĖKĄGĄLDKLĖĄ FĄSKNGĄRF
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RESULT 10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein
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             23-OCT-2003
19-JUN-2003
                                                 ABU37314;
                                                                         ABU37314 standard;
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for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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              (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
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Pred. No. 1.5e-89;
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LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMENLKPPITTTAAAVAYREAILKSL

Query Match Best Local Similarity Matches 192; Conser

Conservative

55;

56.3%;

Score 979; DB; Pred. No. 1.5e. 55; Mismatches

DB 6;

Length

88;

Indels

9

Gaps

62

Sequence

344

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ct the 6213 antisense sequences given in the specification where expression could be determined and inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid cenceding a polypeptide whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid cenceding a polypeptide whose expression is inhibited by the antisense comprising the vector; (3) an isolated controlled acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway considered for proliferation, or that inhibits cellular proliferation; (8) compounds activity; (11) a culture compound that inhibits product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of consideration of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational considered for proliferation in cisolate candidate molecules for rational considered for proliferation in cells other than S. aureus, S. typhimurium, required format directly from MIPO at consideration, but was obtained in electronic format directly from MIPO at
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06-MAR-2002;
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25-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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standardise
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Trawick JD,
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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field)
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Carr G
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Forsyth
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RESULT 11
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                             Wang
Wall
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
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Xu HH;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc proliferation; (7) identifying a compound that influences the activity of cc the gene product or that has an activity against a biological pathway cc required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an cc compound's activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent cc which each of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the cc proliferation of an organism. The antisense nucleic acids are useful for cidentifying proteins or screening for homologous nucleic acids required cr or cellular proliferation to isolate candidate molecules for rational crequired for proliferation in cells other than S. aureus, S. typhimurium, cc required for proliferation in cells other than S. aureus, S. typhimurium, cc patent did not form part of the printed specification, but was obtained cc in electronic format directly from WIPO at cc.
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Matches
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ABO61072
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standard;
                                                                                                                      LPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
                                                                                                                                                          AFLGTDSAPHARHRKEASCGCAGCFNAPTALGSYATVFEEMNALQHFEAFCSLNGPRFYG
                                                                                      LPVNESYVELVREETTVVDSIALPNDTLVPFLAGETVRW
                                                                                                                                                                                     FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
                                                                                                                                                                                                                                 YVRDGNÉ-LLAATITPOHLMFNRNHMLVGGIRPHLYCLPVLKRNIHQQALRELVASGFSR
                                                                                                                                                                                                                                                         FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLFVLKREIHREALVSAVTSGSKR
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                                                                                                                                                                                                                                                                                                          LERMEKLGMPLLVHGEVTHAEIDIFDREARFIETVMEPLRORLPGLKVVFEHITTKDAAE
                                                                                                                                                                                                                                                                                                                                                                                                                   PVDSDENPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLEGKCLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKIRRPDDWHIHLRDDDMLKTVVPYTSEFYGRAIVMPNLVPPVTTVAAAIAYRQRIMDAV
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protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 978; DB 6;
Pred. No. 1.9e-89;
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RESULT 12
ABO61072
ID ABO61072;
XX
AC ABO61072;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide segid 7589.
XX
XX
Example Recombinant expression vector; transcription regulatory element; XX
XX
XX
XX
XX
XX
XX
XX
CS Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX
PN US6610836-B1.
XX
PF 26-AUG-2003.
PF 27-JAN-2000; 2000US-00489039.
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RESULT 13
ABU38565
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic
preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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21-MAR-2002; 2002WO-US009107
                                                                                                                                 Protein encoded
                                                                                                                                                          19-JUN-2003
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                                                  WO200277183-A2
                                                                            Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL
| | :|||||:||| | ::: :|||||||||| ||::::
                                                                                                                                                                                                            standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                            FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKIRRPDDWHIHLRDDDMLKTVVPYTSEFYGRAIVMPNLVPPVTTVAAAIAYRQRIMDAV
                                                                                                                                                                                                                                                                              LPVNESYVELVREETTVVDSIALPNDTLVPFLAGETVRW 348
                                                                                                                                                                                                                                                                                                                                  AFLGTDSAPHARHRKEASCGCAGCFNAPTALGSYATVFEEMNALQHFEAFCSLNGPRFYG
                                                                                                                                                                                                                                                                                                                                                 FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
                                                                                                                                                                                                                                                                                                                                                                                     YVRDGNE-LLAATITPQHLMFNRNHMLVGGIRPHLYCLPVLKRNIHQQALRELVASGFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                          LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGHDFTPLMTCYLTDSLDPAELERGFNEGVFTAAKLYPANATTNSSHGVTST-DAIMPV
                                                                                                                                                                                                                                                                                                      LPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
                                                                                                      prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding a Klebsiella pneumoniae polypeptide, useful vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osborne
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                                                                                                                                                          (first entry)
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                                                                                                                               Prokaryotic essential gene #24092
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                                                                                                      essential
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Pred. No. 1.9e-89;
6; Mismatches 102
                                                                                                      gene;
                                                                                                        cell
                                                                                                      proliferation;
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                                                                                                      drug
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                                                                                                        design
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LQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAVK 182

123

Matches

188;

Conservative

43;

Mismatches

LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKSL

LTLLRPDDWHIHLRDGAALANTVGDAARTFGRAIVMPNLVPPVRNAAEADAYRQRILAAR 64

Similarity

53.8%;

Score 975; DB 6; Pred. No. 3.8e-89;

Length 348;

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123 124 183

LEANAÉVGMPLLVHĞÉVTRAÉVDVFÖRÉKQFIDEHLRVVERFFTLKVVFEHITTGDAAQ
FVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGSKR

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cc the 6213 antisense sequences given in the specification where expression cc of the nucleic acid inhibits proliferation of a cell. Also included are: cc on comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense cc nucleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the cc polypeptide; (5) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway cr agene on which the test compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (12) identifying the target of a compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits or collection of an organism. The target of a compound that inhibits the gene compound that inhibits the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene compound that inhibits the gene c
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
Sequence 348
                                        ftp.wipo.int/pub/published_pct_sequences
                                                              patent did not form part of the printed specification, in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an isolated nucleic acid comprising any one
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Forsyth
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Xu HH;
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RESULT 14
ABO68745
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XX ABO68
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XX Peeud
XX I8-FE
PR 18-FE
PR 27-JU
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XX WPI;
CC FOLOT
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                                                                                                                                                                                                                                      The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and the thereby of pathological conditions, as molecular targets for diagnostics, CC prophylaxis and treatment of pathological conditions resulting from a CC for the ability to bind a P. aeruginosa nucleic acid, as components of CC effective antibacterial targets, as targets for antibacterial drugs, CC production of P. aeruginosa drugs, as templates for recombinant CC components for diagnosis and/or treatment of P. aeruginosa-caused CC infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The CC sequence data for this patent did not form part of the printed CC specification but was obtained in electronic format from USPTO at XXX
                                                                                                                   Query Match
Best Local S
Matches 188
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                                                                                                                                                                                                                    Sequence 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
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27-JUL-1998;
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                                                                                                                                        Similarity
                             LSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMENLKPFITTTAAAVAYREAILKSL
ĹTLLRÞÐÐWHIHLRÐGAALANTVGDAÁRTFGRÁ Í VMÞNLVÞÞVRNAÁEAÐÁÝRQRÍLAAR
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                                                                                                              Conservative
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98US-0094190P
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                                                                                                     Pred. No. 4.7e
3; Mismatches
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Pred. No. 4.7e-89;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid; a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of

Claim 25;

SEQ

ID NO 43220; 1766pp; English.

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RESULT 15
ABU15296
ID ABU15
                                                                                                                      Wang
Wall
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                          21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-CCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #823
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cc required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological cc pathway in which a proliferation required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an cc compound's activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent co which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cc drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. E. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this can electronic format directly from WIPO at figure data for mate directly from WIPO at figure of the printed specification, but was obtained continuation.
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Best Local Similarity 55.8%;
Matches 189; Conservative 4
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LPUNDTFIELUREEQQVAESIALTDDTLVPFLAGETVRW
                                                            LPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
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Search completed: February 12, 2005, 07:02:59 Job time : 96 secs

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PYRC VIBPA
PYRC NEIMA
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6 vibrio para
5 vibrio vuln
6 neisseria m
1 neisseria m
9 vibrio vuln
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chromobacte
vibrio chol
descherichia
pseudomonas
pseudomonas
pseudomonas
pseudomina pe
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yersinia ps
agrobacteri
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shigella fl
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	ALIGNMENTS					
Q9s3sl serratia ma	PYRC_SERMA	ب	204	32.9	596.5	45
4.	Q8D3B4	N	349	38.5	697.5	44
•••	PYRC_BUCAP	μ	349	47.3	856.5	43
	PYRC_BUCAI	۳	350	47.4	859.5	42
0	Q7V896	N	354	49.3	893.5	41
00	Q7VD18	N	359	49.6	899.5	40
	Q7V2B2	N	349		901	39
	Q7U618	N	343		913	38
	Q83B17	N	351		925	37
_	PYRC_RHIME	r	347		931	36
	Q7N5W0	N	350	51.6	935	35
_	Q6FD29	N	344		939.5	34
	PYRC_SALTI	۲	347	52	949	33
	PYRC_SALTY	۲	347	52.5	951	32

Query Match Best Local Matches 2 Q8VXS9; Q8VXS9; 01-MAR-2002 01-MAR-2002 01-OCT-2003 Beta vulgaris (Sugar beet). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta. NCBI_TaxID=161934; Kanhounou R., Serrano R., Ros R.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. -!- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-Dihydroorotase. SEQUENCE FROM N.A. Match 181 121 121 282; 13 61 - \vdash Similarity MELSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILK VLPDDSDFNPLMTLYLTDTTSPNEIKLARKSEVVYAVKLYPAGATTNSQDGVTDLUGKCL VKFVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGS SLPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCL (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 25, 84.3%; ilarity 82.0%; Conservative 3 PRELIMINARY; 34; Created) Last sequence update) Last annotation updat Score 1528; DB 2; Pred. No. 8.8e-116; 4; Mismatches 28; PRT; 345 ₿ update) Length 345; Indels 0 Gaps 180 180 120 120 60 60 240

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KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSENGPDF VKF1ESCNGGNVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKRE1HRQALVSAVTSGS

300 240

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RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., RA Weichneigartner M., de Simone V., Obermaler B., Mache R., Mueller M. Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., RA Weichneigartner M., Puigdomenech P., Watson M., Schmidtheini T., RA Wos P., Hoheisel J., Zimmermann W., Weller H., Ridley P., Vandenbussche F., RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., RA Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., RA Holzer E., Brandt A., Peters S., Van Staveren M., Butter H., Braun M., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Kobetter P., RA Berneiser S., Hempel S., Feldpauch M., Lamberth S., Van den Daele H., RA Petert L., Bysshaert C., Gielen J., Villarroel R., De Clercq R., Lerky M., Lennard N., McLay K., Mayes R., Petert L., Ball S., Kay M., Lennard N., McLay K., Mayes R., Petert L., Rajandream M.A., Lyne M., Bense V., Rechmann S., Rajandream M.A., Lyne M., Bense V., Rechmann S., Rajandream M.A., Lyne M., Bense V., Rechmann S., Ragiriou A., Vitale D., Liguori R., Piravandi E., RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Ra Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., RA Gabel C., Fuchs M., Schmidt W., Lecharmy A., Aubourg S., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Purnelle B., Bent E., Johnson S., Francs P., Belke C., RA Gibbons T., Weber N., Walson R.K., de la Bastide M., Habermann K., RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Francs P., Belke C., RA RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Francs P., Belke C., RA RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Francs P., Belke C., RA RA Perez-Perez A., Purnell B., Granderath K., Bastide M., Habermann K., Bentley D., Fulton B., Maller N., Scott K., Johnson D., Lencke K., Mew
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Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20083488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dihydroorotase."
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-25-007-2004 (Rel. 45, Last annotation update)
Dihydroorotase, mitochondrial precursor (EC 3.5.2.3) (DHOase).
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10617198; DOI=10.1038/47134;
ueller C., Wambutt R., Murphy G., vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Arabidopsis thaliana cDNA encoding
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PROSITE; PS00483; DIHYDROOROTASE 2; 1.
PROSITE; Metal-binding; Mitochondrion; Pyrimidine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004721; DHOdimr. —
InterPro; IPR002195; Dihydroorotase.
Pfam; PF01979; Amidohydro_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF000146; AAB71134.1; -. EMBL; AL031018; CAA19808.1; -. EMBL; AL161558; CAB79248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C. Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R. Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M.A., Martienssen R., McCombie W.R.; "Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006680; Amidohydro 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402:769-777(1999).
-i- CATALYTIC ACTIVITY: (S)-dihydroorotate +
       301
                                  273
                                                          241
                                                                                     213
                                                                                                             181
                                                                                                                                        153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: Binds 2 zinc ions per subunit (PATHWAY: Pyrimidine biosynthesis; third subcellular LOCATION: Mitochondrial (Pote SIMILARITY: Belongs to the DHOase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aspartate.
COFACTOR: Binds 2 z:
PATHWAY: Pyrimidine
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                                                                                                                                                                                                                                               33
                                                                                                                                                                                                                                                                                                    269;
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                  SLPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCL
YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDWLP
                      KKFFLGTDSAPHEKSKKESSCGCAGIYSAPIALSLYAKVFDEAGALDKLEAFTSFNGPDF
                                       KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDF
                                                                           VNFVESCKEGSVGATVTPQHLLLNRNALFQGGLQPHNYCLPVLKREIHREAIVKAVTSGS
                                                                                         VKFVESCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYGLPVLKREIHREALVSAVTSGS
                                                                                                                              PVLEEMVKQNMPLLVHGSVTDPSIDVFDREKIFIETVLQPLIQRLPQLKVVMEHITTMDA
                                                                                                                                               PVLQEMVEHNMPLLVHGEVTNDEVDMFDREKVF1ETVLRPLVQKFPQLKVVMEHVTTIDA
                                                                                                                                                                                  TIGRO0856; pyrC_dimer; 1.
PS00482; DIHYDROOROTASE 1;
PS00483; DIHYDROOROTASE_2;
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46
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78.4%;
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Dihydroorotase.
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 1 and 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
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Pred. No. 9e-111;
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R GO; GO:0004151; F:ddinydroorotase activity; IEA.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0019656; P:pyrimidine base biosynthesis; IEA.

R GO; GO:0019656; P:pyrimidine base biosynthesis; IEA.

R InterPro; IPR006680; Amidohydro_1.

R InterPro; IPR004721; DHOdimr.

RR InterPro; IPR002195; Dihydroorotase.

Pfam; PF01979; Amidohydro_1; 1.

DR TIGRPAMs; TIGR00856; DyrC dimer; 1.

DR TIGRPAMs; TIGR00856; DyrC dimer; 1.

DR PROSITE; PS00482; DIHYDROOROTASE 1; UNKNOWN_1.

DR PROSITE; PS00483; DIHYDROOROTASE 2; 1.

KW Hydrolase; Metal-binding; Pyrimidine biosynthesis; Zinc.

KW Hydrolase; Metal-binding; Pyrimidine biosynthesis; Zinc.
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RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Hosokawa S., Mao T., Aoki H., Arita K., Hamada M., Haradda C.,
RA Ikano M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y.,
RA Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
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Q1-DEC-2001
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Name=P0481E12.10;

Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COPACTOR: Binds 2 zinc ions per subunit (By similarity)
-!- PATHWAY: Pyrimidine biosynthesis; third step.
-!- SIMILARITY: Belongs to the DHOase family.
EMBL; AP003076; BAB56025.1; -.
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PubMed=12447438; D
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Gramene; Q94J;
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VLEEMARQEMPLLVHGEVTDQHVDTFDREKVFIEKILAPLVQRLPQLKIVMEHITTMDAV
                                     VLQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAV
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GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; E:hydrolase activity; IEA.
GO; GO:0019856; P:pyrimidine base biosynthesis; IEJ
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR004721; DHOdimr.
InterPro; IPR002195; Dihydroorotase.
PF01979; Amidohydro_1; 1.
TIGRNAMS; TIGR00856; PYCC dimer; 1.
PROSITE; PS00483; DIHYDROOROTASE_1; 1.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
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Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L./
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
"Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautotroph Nitrosomonas europaea.";
J. Bacteriol. 185:2759-2773(2003).
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MEDLINE=22586410; PubMed=12700255;
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349 AA; 39083 MW;
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HSSP; P05020; 1J79.
HAMAP; MF 00219; -; 1.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR002195; Dihydroorotase.
Pfam; PF01979; Amidohydro_1; 1.
TIGRPAMs; TIGR00856; pyrC_dimer; 1.
PROSITE; PS00482; DIHYDROOROTASE_1; 1.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
Complete proteome; Hydrolase; Metal-binding; Pyrimidine biosynthesis;
Complete proteome; Hydrolase; Metal-binding; Pyrimidine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21681879; PubMed=11823852; DOI=10.1038/415497a; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "CarnLyTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-
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Q8Y249;
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28-FEB-2003 (Rel. 41, Last sequence update)
95-JUL-2004 (Rel. 44, Last sequence update)
95-JUL-2004 (Rel. 44, Last annotation update)
Dihydroorotase (EC 3.5.2.3) (DHOase).
Name=pyrC; OrderedLocusNames=RSC0487; ORFNames=RS
Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiaceae; Ralstonia.
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STRAIN=GMI1000;
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COFACTOR: Binds 2 zinc ions per subunit (By similarity)

PATHWAY: Pyrimidine biosynthesis; third step.

SUBUNIT: Homodimer (By similarity).

SIMILARITY: Belongs to the DHOase family. Subfamily 1.
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          Score 1061; DB
Pred. No. 8e-78;
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Q62H45;
Q62H45;
Q5-CCT-2004 (TrEMBLrel. 28, Created)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Dihydrocrotase, homodimeric type (EC 3.5.2.3).
Name=pyrC, ORFNames=BMAY422;
Burkholderia mallei ATCC 23344.
Bacteria; Proceobacteria; Betaproteobacteria; Burkholderianese; Burkholderia.
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    YVRDADAASGRIGATITAHHLLYNRNAMFFGGIRPHYYCLPVLKRETHRJ
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Pred. No. 1.5e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence upda
25-OCT-2004 (TrEMBLrel. 28, Last annotation up
Dihydroorotase (EC 3.5.2).
Name=pyrC; ORFNames=BPSU2914;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL; EX571965; CAH36924.1; -.
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25-OCT-2004
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|:::|||||||:||:||:|:||:||:||:||:||||:::
LTLARPDDWHLHVRDGAMLAAVLPHTARQFGRAIIMPNLKPPVTTTAQAQAYRERILAAV
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                                                                                                                                                                                                                                                                                                                                                                                  LQEMVEHNMELLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDÄVK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLPV 122
                                                                                                                                                                                                                                                                       FVE--SCTEGFVAATVTPQHLVLNRNSLFQGGLQPHNYCLPVLKREIHREALVSAVTSGS
                                                                                                                                                                                                                                                                                                                                                   LEAMOEVGMPLLVHGEVTDPSIDLFDREKVFIDRVMEPLRRALPGLKVVFEHITTKDAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGMTFEPLMTLYLTDNTPADEIRRARESGCVHGVKLYPAGATTNSDAGVTDLLGKCAKT 128
                                                       YGLPRNNSKIKLSKTPWKVPESFSYASGDIIPMFAGEMLDW 341
                                                                                                                                                                     KRFFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDF 300
                                                                                                                                                                                                                                     YVRDADAASGRIGATITAHHLLYNRNAMFFGGIRPHYYCLPVLKRETHRIALVEAATSGN
                                                                                                                 PRFFLGTDSAPHAKGAKEAACGCAGCYTALHALELYAEAFDQAGALDKLEGFASFFGADF
YGLPRSAETVTLRRETWELPREIDAGAGPVVPLRGGEAIGW
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1058; DE
Pred. No. 1.5e-
15; Mismatches
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   349
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Matches 200
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PIR; S76410; S76410.

HSSP; PD5020; 1J79.

HAMAP; MF_00219; -; 1.

InterPro; IPR006680; Amidohydro_1.

InterPro; IPR004721; Dihydroorotase.

Pfam; PF01979; Amidohydro_1; 1.

Pfam; PF01979; Amidohydro_1; 1.
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P74438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97061201; PubMed-8905231;
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nak
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K.
Hosouchi T., Matsuno A., Watanabe A., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions." DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-pyrC; OrderedLocusNames=s1r0406;
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation updat
Dihydroorotase (EC 3.5.2.3) (DHOase).
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                                                                                                                                                                                                                                                                                                             TIGREAMS; TIGR00856; pyrC_dimer; 1.
PROSITE; PS00482; DIHYDROOROTASE_1;
PROSITE; PS00483; DIHYDROOROTASE_2;
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                               Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (Seend an email to license@isb-sib.ch).
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SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the DHOase family. Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: Binds 2 zinc ions
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  122
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                                                                                                                                                 Similarity
                                                                                              ELSITQPDDWHLHLRDGDVLKAVVSHSAHHFGRAIVMPNLKPPITTTAAAVAYREAILKS
                                                                                                                                                                                                                                                                                                proteome;
                                                                               VLQEMVEHNMPLLVHGEVTNPEVDMFDREKVFIETVLRPLVQKFPQLKVVMEHVTTIDAV
                             IPAGGQFEPLMTLYLTDNTNPEEIIAAKASQFVKAVKYYPAGATTNSDFGVTDIH-RCDA
                                         LPVDSDFNPLMTLYLTDTTSPMEIKLARESQVVFGVKLYPAGATTNSQDGVTDLFGKCLP
                                                                                                                                                                                                   13
99
136
136
174
                                                                                                                                    Conservative
                                                                                                                                                                                        AA;
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15
99
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174
246
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38127
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Zinc
Zinc
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Zinc
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Pred. No. 1.9e-77;
2; Mismatches 85
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Zinc 1 (By similarity).
Zinc 1 and 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
EBA572814296B121 CRC64;
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ASE_2; 1.
Metal-binding; Pyrimidine
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nesis; third step.
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                                                                                                                                                               DB 1;
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RC STRAIN=ATCC 12472 / DSM 30191;

RX MEDLINE=22882880; pubmed=14500782; DOI=10.1073/pnas.1832124100;

RA Antonio R.V., Almeida F.C., de Almeida D.F., de Almeida R.A.,

RA Antonio R.V., Almeida F.C., de Almeida LG.P., de Almeida R.A.,

RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

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RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Camargo A.A., Cardoso D.D.P., Carrario L.N.P., Carraro D.M.,

RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,

RA Carratho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Fantinatti F., Farias I.P., Felips M.S.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.I.T., Franco G.R., Freitas N.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.I.T., Franco G.R., Freitas N.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.I.T., Franco G.R., Freitas N.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.I.T., Franco G.R., Freitas N.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.I.T., Franco G.R., Freitas N.S., Ferrari L.P., Ferro J.A.,

RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Gazzinelli R.T., Loureiro M.F., Lyra M.C.C. P.,

RA Grattapaglia D., Jane M.F., Jane M.F., Jardim S.N., Laurino J.,

RA Grattapaglia D., Lima L.F.A., Loureiro M.F., Lyra M.C.C. P.,

RA Mascimento F.F., Nicolas M.F., Oliveira S., Jardim S.N., Leurino J.,

RA Mascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,

RA Mascimento F.F., Santos F.R., Schmeider M.P.C., Seuanez H.N.,

RA Mascimento F.F., Sant
    aspartate.

-!- COFACTOR: Binds 2 zinc ions per subunit (By similarit;
-!- PATHWAY: Pyrimidine biosynthesis; third step.
-!- SIMILARITY: Belongs to the DHOase family. Subfamily 1
EMBL; AE016925; AAQ61989.1; -.
R EMSL; P06020; 1J79.
R GO; GO:0004151; F:dihydroorotase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016787; F:hydrolase biosynthesis; IEA.
R GO; GO:0006221; P:pyrimidine base biosynthesis; IEA.
R GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유 상 유
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Q7NQ12;
01-MAR-2004
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Dihydroorotase (EC 3.5.2.3).
Name=pyrC; OrderedLocusNames=CV4330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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Amidohydro_1
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                                                                                                                                   Subfamily
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Best Local (
     This
                                                                                                                           SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / Serotype 01;

MEDLINE=20406833; PubMed=1952301; DOI=10.1038/35020000;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,

Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,

Nlerman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,

Mekalanos J.J., Venter J.C., Fraser C.M.,

"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                       Nature 406:477-483(2000).
-i- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                         PYRC VII
Q9KL24;
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
25-CCT-2004 (Rel. 45, Last annotation
Dihydroorotase (EC 3.5.2.3) (DHOase).
                                                                                                                                                                                                                                                                                                                 Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                       Name=pyrC;
                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae.
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InterPro; IPR002195; Dihydroorotase.
Pfam; PF01979; Amidohydro 1; 1.
TIGRPAMS; TIGR00856; pyrc_dimer; 1.
PROSITE; PS00483; DIHYDROOROTASE 2;
Complete proteome; Hydrolase; Metal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                     SIMILARITY: Belongs to the DHOase family. Subfamily 1.
                                     aspartate.

COFACTOR: Binds 2 zinc ions per su COFACTOR: Binds 2 zinc ions per su COFACTOR: Byrimidine biosynthesis; SUBUNIT: Homodimer (By similarity)
    SWISS-PROT
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proteome; Hydrolase; Metal-binding; Pyrimidine
                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=VCA0925;
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  entry
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osynthesis; third
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Pred. No. 3.8e-
46; Mismatches
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19
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                                                             similarity)
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RESULT 11

QGLP1
ID QGLP1
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Best Loc
Matches
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OS-JUL-2004 (TrEMBLrel. 27, Created)
OS-JUL-2004 (TrEMBLrel. 27, Last Bequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative dihydroorotase.
Name=CV4330; OrderedLocusNames=PBPRA2405;
Photobacterium profundum (Photobacterium sp. (strain SS9)).
Photobacterium croteobacteria; Gammaproteobacteria; Vibrionales;
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TIGR; VCA0925; ...

HAMAP; MF_00219; .; 1.

InterPro; IPR006680; Amidohydro_1.

InterPro; IPR004721; DHOdinr.

InterPro; IPR002195; Dihydroorotase.

Pfam; PF01979; Amidohydro_1; 1.

Pfam; PF01979; Amidohydro_1; 1.

TIGRPAMs; TIGR00856; pyrC_dimer; 1.

PROSITE; PS00482; DIHYDROOROTASE_1; 1.

PROSITE; PS00483; DIHYDROOROTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                            LPRNQETVILTKQAWPVAESMPFGSDIVVPIRAGENIEW
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Zinc 1 (By similarity).
Zinc 1 and 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
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Pred. No. 4.5e-
45; Mismatches
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  Simonato
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  Ή
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GO; GO:0004151; F:ddihydroorotase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0019856; P:pyrimidine base biosynthesis; IEA.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR004721; DHOdimr.
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InterPro; IPR004721; DHOdimer; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Dihydroorotase (EC 3.5.2.3).
Name=pyrC; OrderedLocusNames=BPD3762;
Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria
STRAIN=12822 / ATCC BAA-587,

MEDLINB=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINB=22827954; PubMed=12910271; DOI=10.1038/ng1227;

Parkhill J., Sbbaihia M., Preston A., Murphy L.D., Thomson N.R.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
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PS00482; DIHYDROOROTASE 1;
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"Comparative analysis of the genome sequences of Bordetella pert

"Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35.32-40(2003).

"REMBL; BX640434; CAE39045.1; -.

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OTWFR2;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (EC 3.5.2.3).
Name=pyrC; OrderedLocusNames=BB4208;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria; Betaproteobacteria; Burkholderiales;
alcaligenaceae; Bordetella.
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RESULT 14
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Q7VUP3;
Q7VUP3;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seque)
01-MAR-2004 (TrEMBLrel. 26, Last annot.
Dihydroorotase (EC 3.5.2.3).
Name-pyrC; OrderedLocusNames=BP3035;
Bordetella pertussis.
Bacteria; Proteobacteria; Betaproteobachlocuslationalis (PC 3.5.2.3).
NCBI TaxID=520;
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GO; GO:0004151; F:dihydroorotase activity; IEA
GO; GO:0016787; F:hydrolase activity; IEA
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0019856; P:pyrimidine base biosynthesi
InterPro; IPR006680; Amidohydro 1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR004721; DHOdimr.
InterPro; IPR002195; Dihydroorotase.
Pfam; PF01979; Amidohydro 1; 1.
TIGRFAMS; TIGR00856; pyrC_dimer; 1.
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COMplete proteome.
SEQUENCE 359 AA; 38969 MW; A75138BCEOC7DE
SEQUENCE FROM N.A.

STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

Parkhill J., Sebalhia M., Preston A., Murphy L.D., Thomson N.R., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unwin I., Whitchead S., Barrell B.G., Maskell D.J.; "Comparative analysis of the genome sequences of Bordetella Bordetella parapertussis and Bordetella bronchiseptica."; Nat. Genet. 35:32-40(2003).
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Pred. No. 7.4e-
16; Mismatches
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Best Local 9
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GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0019856; P:pyrimidine base biosynthesis; IE.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR004721; DHOdimr.
InterPro; IPR002195; Dihydroorotase.
InterPro; IPR002195; Dihydroorotase.
IPS003175; PS00482; DIHYDROOROTASE_1; 1.
PROSITE; PS00482; DIHYDROOROTASE_2; 1.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
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RMBL; BX640420; CAE43304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 Q8EB40
QBEB40;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
MEDLINE-22297686; PubMed=12368813; DOI=10.1038/nbt749; Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J., Brinkac L.M., Daugherry S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Shewanellaceae; Shewanella
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                           Name=pyrC; OrderedLocusNames=SO3695;
Shewanella oneidensis.
Bacteria: partire
                                                                                                                                                                                  SEQUENCE FROM N.A.
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359 AA; 39013 MW;
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                                                                                                                                                                                                                                                                                        Gammaproteobacteria;
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Pred. No. 1.6e-73;
6; Mismatches 97;
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Last annotation updat
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Matches 190
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GO; GO:0004151; F:dihydroorotase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0019856; P:pyrimidine base biosynthesis; IE;

GO; GO:0019856; P:pyrimidine base biosynthesis; IE;

InterPro; IPR006680; Amidohydro_1.

InterPro; IPR004721; DHOdimr.

InterPro; IPR004721; Dihydroorotase.

Pfam; PF01979; Amidohydro_1; 1.

TIGRFAM6; TIGR00856; DYC Cdimer; 1.

PROSITE; PS00483; DIHYDROOROTASE_1; 1.

PROSITE; PS00483; DIHYDROOROTASE_2; 1.

Complete proteome.
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Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M.,
Utterback T.R., McDonald L.A., Feldblyum T.V., Smith
Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reduce Shewanella oneidensis.";
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HSSP; P05020; 1J79.
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                                                                                                                                LPRNSDTITLVKKAWDIPASYPLGDTNVVPIRAGEQIDW
                                                                                  FFLGTDSAPHDRRRKECSCGCAGIYNAPVALSVYAKVFEKENALDKLEAFTSFNGPDFYG
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SUMMARIES

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242.6 241 241 238.2	267.4 264.2 264.4 264.2 245.6 245.6	1271 1271 646 281 281 277.2 272.8 272.8 272.8	Score
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ABD02437 ACA42435 ACA27332	ACA20646 ADA30128 ACA26372 ACA24115 ABA92787 3 ACA19166 ADA02724 ABD02716	AAF61217 AAF61262 AAL44159 ACA53620 ACA53620 ACA54350 ACF68579 ACF67367_13 ACF665379	ID
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This invention describes a novel use of a DNA sequence (I) encoding dihydro-orotase (II) to prepare plants which have increased

Claim 3; Page 28-30; 32pp; German.

Increasing the polysaccharide, especially starch, content of plants, by transforming with a sequence encoding dihydro-orotase.

WPI; 2001-202938/20. P-PSDB; AAB70773.

Ehrhardt T, Stitt Nigel M, Schroeder M;

Geigenberger PL,

Loef I,

Zrenner R;

12-AUG-2000; 2000WO-EP007884

20-AUG-1999; (BADI) BASF

99DE-01039688

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ALIGNMENTS

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RESULT 1
AAF61217
ID AAF6
AAF61217 standard; cDNA; 1271 BP
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                                                                                                                                                                                              Potato dihydro-orotase cDNA.
                                                                                                                                                                                                                     AAF61217;
                                                                                                                01-MAR-2001.
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                                                                                                                                                                  Solanum tuberosum.
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/product= "dihydro-orotase"
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Query Match
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New DNA encoding plant dihydroorotase, plants and for screening for compounds
                                                    WPI; 2001-235198/24.
P-PSDB; AAB70779.
                                                                                                                                                                            02-SEP-2000; 2000WO-EP008581
                                                                                                                                                                                                                                                                                                                                                                Potato; dihydro-orotase; inhibitor; herbicide; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                  dihydro-orotase cDNA.
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                                                                                                                               Sugar beet, gene, ds, transgenic plant, osmotic stress tolerance, oxidative stress tolerance, casein kinase alpha catalytic subunit, dihydroorotase, translation initiation factor IA, plant flowering, plant growth stimulation.
           04-JUL-2002
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                                WO200252012-A2
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                                                      "Beta vulgaris dihydroorotase'
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Best Local Similarity
Matches 793; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of sugar beet (Beta vulgaris) genes that are involved in osmotic and oxidative stress tolerance in a plant. The Beta vulgaris genes of the invention encode the proteins: casein kinase alpha catalytic subunit; dihydrocrotase; protein. The Beta vulgaris genes of the invention are useful for enhancing the osmotic and oxidative stress tolerance of a plant. The Beta vulgaris genes of the invention are useful for vulgaris genes are also useful for stimulating plant growth. The casein of flowering in a plant. The precess vulgaris dihydrocrotase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel sugar beet genes involved in stress response, useful for rendering crops resistant to stress situations like osmotic stress caused by salt, drought, cold or frost thus increasing crop yield.
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DB; AAO15493.
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New antisense nucleic acids, for homologous nucleic acids
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useful for identifying proteins or required for cellular proliferation

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RESULT 4
ACA53620
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Wall
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
P-PSDB;
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                                                                                                                                                                                                                 03-OCT-2002.
                                                                                                                                                                                                                                                                    Vibrio cholerae
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Yamamoto R,
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Forsyth
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Xu HH;
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CC encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated concleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the carried or its fragment whose expression is inhibited by the concleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular conclideration or the activity of a gene in an operon required for proliferation; (7) identifying a compound that infibences the activity of identifying a gene required for cellular proliferation; (8) congular macts; (9) manufacturing an activity against a biological pathway capanism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an congular macts; (12) manufacturing an antibiotic; (12) profiling a compound that inhibits proliferation of an congular mactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is overexpressed or underexpressed; (12) determining the extent conduct is proliferation of a culture compound that inhibits the gene product is proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required conduct for proliferation to isolate candidate molecules for rational conduct for proliferation in cells other than S. aureus, S. typhimurium, content form part of the printed specification, but was obtained in the printed specification, but was obtained in
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Best Local
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) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         local Similarity
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Best Local S
Matches 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to new Proteus mirabilis polypeptides and polypuncleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunishing an individual against p. mirabilis method for evaluating a compound for the ability to bind a p. mirabilis activity. The polypeptides and polypuncleotides are useful as molecular resulting from bacterial infection, as reagents for diagnosing, preventing and treating pathological conditions bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a proteus mirabilis polynucleotide of the invention.
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                           TTTTTTCTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAAAGAGTGTTCTTGTGGA
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Pred. No. 9.9e-71
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                           Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                               Prokaryotic essential gene
                                                                                                                                                                                                                                                                                                                                          drug design;
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Carr GJ,
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Xu HH;
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New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. ő

ID NO 42220; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC encoding a polypeptide whose expression is inhibited by the nucleic acid culcic acid; (2) a host cell containing the vector; (3) an isolated CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense CC polypeptide; (3) producing the polypeptide; (6) inhibiting cellular CC proliferation, or the activity of a gene in an operon required for containing the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular CC proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) cc identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies

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cc organism acts; (9) manufacturing an antiblotic; (10) profiling a cc compound's activity; (11) a culture comprising strains in which the gene cc compound's activity; (11) a culture comprising strains in which the gene cc product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of cc strains; or (13) identifying the target of a compound that inhibits the cc proliferation of an organism. The antisense nucleic acids are useful for cidentifying proteins or screening for homologous nucleic acids required cc for cellular proliferation to isolate candidate molecules for rational cd discovery programs, or for screening homologous nucleic acids crequired for proliferation in cells other than S. aureus, S. typhimurium, C. K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did cont form part of the printed specification, but was obtained in celectronic format directly from WIPO at
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The invention relates to the isolation of genes and their encoded cc proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens cc and related species; to study polymorphisms; for gene analysis and for cd detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification cc of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that cc animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. cc luminescens. Cells transformed to express the genes are useful for crecombinant production of the proteins, particularly toxins and cc antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and bacteria or fungit that the containing the genes and selection of that also useful the containing the genes and selection of the proteins.
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Buchrieser
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Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;

Photorhabdus luminescens.

2002WO-IB003040

07-FEB-2001; 2001FR-00001659

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Genomic sequence of Photorhabdus luminescens useful e.g. as therapeutic antimicrobials and Claim 1; SEQ ID NO 32; 1205pp; French. and and and encoded polypeptides, agricultural pesticides.

The invention relates to the isolation of genes and their encoded CC proteins from Photorhabdus luminescens. The isolated sequences are CC sources of probes and primers for detecting the genome of P. luminescens CC and related species; to study polymorphisms, for gene analysis and for CC detection/amplification of the genes. Antibodies (Ab) raised against the CC polymeptides encoded by the genes are used for detection/identification CC polymeptides encoded by the genes are used for detection/identification CC control of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that CC carry a gene-containing vector are used to select compounds that CC carry a gene-containing the toxins and antibiotics produced by P. CC undinals or microorganisms other than P. luminescens and are able to alter CC response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for CC entibacterials useful as insecticides, particularly toxins and CC entibacterials (to treat microbial infection by bacteria or fungi that CC genes, proteins, vectors containing the genes and Ab are also useful CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as dispositive to P. luminescens-encoded toxins or antibiotics) and as dispositive to P. luminescens-encoded toxins or antibiotics) and as dispositive to P. luminescens-encoded toxins or antibiotics) and as dispositive to P. luminescens-encoded toxins or antibiotics) and as dispositive to P. luminescens-encoded toxins or antibiotics) and as dispositive to P. luminescens encoded toxins or antibiotics) and as dispositive to P. luminescens encoded toxins or antibiotics) and as dispositive to P. luminescens encoded toxins or antibiotics) and as dispositive to P. luminescens encoded toxins or antibiotics) and as dispositive to P. luminescens encoded toxins or antibiotics) and as dispositive to P. luminescens encoded toxins or antibiotics). This cc.

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       Antisense; ds; prokaryotic drug design; gene.
                                              Prokaryotic essential gene
                                                                                                                               ACA20646 standard; DNA; 1032 BP
                                                                              19-JUN-2003
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                                                                             (first
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           essential gene; cell proliferation;
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Query Match Best Local S Matches 540

Similarity

21.0%;

540;

Conservative

0,

Score 267.4; DB 8; Pred. No. 8.7e-67; 0; Mismatches 411;

Length 1032;

6

81 86

27

Sequence 1032 BP;

309 A; 210 C;

205 G; 308 T; 0 U; 0 Other;

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The invention relates to an isolated nucleic acid comprising any one of CC of the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid compounds a polypeptide whose expression is inhibited by the antisense compound in the linked to the nucleic acid compounds and isolated compounds of the polypeptide of specifically binding compounds in inhibited by the antisense compounds in inhibited by the antisense compounds in inhibited by the compounds of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular compounds that influences the activity of agene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation or that has an activity against a biological pathway in which a proliferation required gene or its gene product lies compound that inhibits proliferation of the compound that inhibits proliferation of a compound's activity, in culture comprising strains in which the gene compound's activity, in culture comprising strains in which the gene compound's activity, in an antibiotic; (10) profiling a compound's activity, in culture comprising strains in which the gene compound's activity, in the target of a compound that inhibits proliferation of the strains is present in a culture or collection of compound's activity in the target of a compound that inhibits the extent strains; or (13) identifying proteins or screening for homologous nucleic acids are useful for compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Wall D,
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00742851.

06-MAR-2002; 2002US-0362699P.
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DB; ABU16776.
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Forsyth
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ADA30128
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                                                          gene; Acinetobacter baumannii; bacterial disease;
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                                                                                         Acinetobacter baumannii protein
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                 baumannii
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386 327 326 267 266 207 206 147 146 87

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AAACTTAAAGTTGTGCTTGAGCACATCACTACCAGTGATGCAGCACACTTTGTT--

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Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1041 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGGTTCTTAAGGCAGTTGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1415; 328pp; English
                                                                                                                                                                                                                                                     GATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTCCTATGGAAAATCAAA
                                                                                                                                                                                                                                                                                                                                                          GATTTGGCTAAACAATTCGCCCGCGCGATTTGTATGCCTAACCTTGTACCGCCTGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                   CACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAAGCCTCCTATCACT
                                                                                                                                                             ARAATTAAAGAATCAGAACATGTAAATGCGATTAAGCTTTATCCTGCTGGTGCGACCACA
                                                                                                                                                                                                                                                                                                                        ACCACTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTTTACCTGTTGATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGTGCAGAAATTTCCA
                                  GAAGAGCATCAAGTTCCGTTATTGCTTCATGGTGAAGTAACTCATAATCATGTAGATATT
                                                               GTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGTTACTAATCCTGAGGTTGACATG
                                                                                                 AACTCCGATAATGGTGTGAGTGATATT---CGTAAAGTTTATGCAGTCATTGAGCAATTA
                                                                                                                       AATTCTCAAGATGGAGTGACCTGATCTTTCGGGAAGTGTTTACCAGTTCTACAAGAAATG
                                                                                                                                                                                 CTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCTGGTGCCACGACA
                                                                                                                                                                                                                            AATTTTGACCCTCGTATGGTGCTTTATTTTACTGACCACACTTCACCTGATGAAGTTCGT
                                                                                                                                                                                                                                                                                           ACAGTAGAAGAAGCTTTAGCTTATCGCGAACGCATTCTTGCTCATGTTCCGGAAGGCAAT
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Pred. No. 8.8e-67;
0; Mismatches 411;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression
                                          Claim 14;
                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                 03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                 Antisense; ds; prokaryotic drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                 Prokaryotic essential gene #8029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACA26372 standard; DNA; 1056
                                                                                                                                                                                                                                                                                                                                           Burkholderia mallei.
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Trawick
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                    NO 14242; 1766pp; English.
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                                                                                                                                           Malone C,
Carr GJ,
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Yamamoto R,
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Forsyth
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the nucleic acid inhibits proliferation of a cell. Also included are:
(C) (1) a vector comprising a promoter operably linked to the nucleic acid
(C) encoding a polypeptide whose expression is inhibited by the antisense
(C) contest acid; (2) a host cell containing the vector; (3) an isolated
(C) antisense nucleic acid; (4) an antibody capable of specifically binding
(C) contiseration or the activity of a gene in an operon required for
(C) proliferation; (7) identifying a compound that influences the activity of
(C) required for proliferation, or that inhibite cellular proliferation; (8)
(C) compound's gene required for cellular proliferation or the biological
(C) pathway in which a proliferation or that inhibite cellular proliferation; (8)
(C) compound's activity; (11) a culture dene or its gene product of
(C) compound's activity; (11) a culture comprising strains in which the gene
(C) product is overexpressed or underexpressed; (12) determining the extent
(C) strains; or (13) identifying an antibiotic; (10) profiling a
(C) product is overexpressed or underexpressed; (12) determining the extent
(C) to which each of the strains is present in a culture or collection of
(C) proliferation of an organism. The antisense nucleic acids required
(C) did iscovery programs, or for screening homologous nucleic acids required
(C) compound activity in the same nucleic acids are useful for
(C) compound activity in the same nucleic acids are useful for
(C) compound activity in the same nucleic acids are useful for
(C) compound activity in the same nucleic acids are useful for
(C) proliferation of an organism. The antisense nucleic acids required
(C) did iscovery programs, or for screening homologous nucleic acids required
(C) compound activity in the same antisense nucleic acids required
(C) prokaryotic essential genes. Note: The sequence is one of the target
(C) prokaryotic essential genes. Note: The sequence data for this patent did
(C) compound the compound that inhibits the sequence data for this patent did
(C) prokaryot
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                                                                     GCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTAA
                                                                                                                     TGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGT 493
             GTTTGT----
                                                                                                                                                                                                     GCTCGAGGCGATGCAGGAAGTCGGGATGCCGCTGCTGCTGCACGGCGAGGTGACGGATCC
                                                                                                                                                                                                                               TCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGGTTACTAATCC
                                                                                                                                                                                                                                                                                   GGGCGCGACGACTCGGACGCCGGCGTGACCGACCTGCTCGGCAAGTGCGCGAAGAC
                                                                                                                                                                                                                                                                                                             TGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGT 373
                                                                                                                                                                                                                                                                                                                                                                    CGACGAAATCCGCCGCGCACGCGAAAAGCGGCTGCGTGCACGGCGTGAAGCTCTATCCGGC
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-TGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCACAACA
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Pred. No. 3.8e-66;
0; Mismatches 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
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isolate candidate molecules for rational drug discovery programs

14; SEQ ID NO 11985; 1766pp; English

the fall antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(C) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense comprising the vector; (3) an isolated complete acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway capable of specifically binding cellular proliferation; (7) identifying a compound that influences the activity of agene product or that has an activity against a biological pathway capable of specifical pathway in which a proliferation, or that inhibits proliferation or the biological pathway in which a proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collular proliferation of culture comprisins in which the gene proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational conditions or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target corrolled form part of the printed specification, but was obtained in cellectronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences invention relates to an isolated nucleic acid comprising any one of

Sequence 1092 BP; 175 A; 396 C; 362 G; 159 ij, o u; 0 Other;

Matches Best Local Similarity Query Match 540; Conservative 20.8%; Score 264.4; DB 8 Pred. No. 6.7e-66; 0; Mismatches 411 411; 8 Length 1092; Indels 9; Gaps N

밁 á 밁 8 문 S 밁 Ş Ś 밁 á 밁 δ 밁 S 밁 314 123 420 374 363 303 254 243 194 183 134 480 434 14 74 63 GGCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAA 133 GCTCTCAATCACAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTAA TATGGAAATCAAACTAGCAAGAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGC GCCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTTT ceccerecreciecacacacecececaerreeececececerareereareceaacereaa TGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGT CGACGAAATCCGCCGCGCGCGCGAAAGCCGGCTTCGTGCACGGCGTGAAGCTGTATCCGGC ACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTCC GCTTTCGCTCGCCCGTCCCGACGACTGGCACCTGCACCTGCGAGACGGCGACATGCTCGC GTCGATCGACCTGTTCGACCGCGAGAAGGTGTTCATCGACCGCGTGATGACGCCGCTGCG TGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGT TCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGCTGCTTCATGGAGAGGGTTACTAATCC AGGCGCCACGACGAATTCCGACCATGGCGTCACCGATC---TCGCGAAATGTGCGAAGAC GCCGGCCGGGATGACGTTCGAGCCGCTGATGACGCTGTACCTGACCGACAACACGCCGCC GCCGCCGGTCACGACCACCGCGCAGGCGCAGGCGTATCGCGAGCGCATCCTCGCCGCGCT 122 479 419 313 302 253 193 182 73 493 433 373 362 242 539

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                                                                          GAATTATAAATTCAAACCGTTAATGACTTGTTATTTAACTAATTCCACAAGCCCTAAAGA
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                                 ACTAGAATTTGGTTTTTCTÄAAAAAATATTTGTAGCAGCTAAATTCTATCCAAATGGTTG

        PATCAPACTAGCABGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCTGGTGC

                                                                                                                   GATTACGAGTTGTTTGAAAAAGCATTGCGTATCGTAATAGAATTTTAAAAATCAATGCACTT
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21-MAR-2001; 21-MAR-2002; 2002WO-US009107 Escherichia coli Antisense; ds; prokaryotic essential drug design; gene. Prokaryotic essential 19-JUN-2003 ACA19166 standard; 2001US-00815242 (first DNA; entry) gene 1047 #823 ВP gene; cell proliferation;

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cc (1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated congregation or its fragment whose expression is inhibited by the antisense comprising a polypeptide whose expression is inhibited by the antisense compression or its fragment whose expression is inhibited by the continuous control of the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular control or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of confidenciating identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confidentifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation or screening for homologous nucleic acids are useful for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs
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Sequence 1415, Application US/09328352
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Pred. No. 1.4e-73;
0; Mismatches 411;
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Sequence 1, Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HORMI
I APPLICANT: SAKAKI, YOSHIYUKI
ITITLE OF INVENTION: GENOME DNA OF BACTERIAL SYN
IFILE REFERENCE: 081356/0159
CURRENT PILICATION NUMBER: US/09/790,988
CURRENT PILICATION NUMBER: US/09/790,988
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
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                                                                                        TGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTTTATGGGCTTCC
                                                                                                                                GGGTATATTTAATGCTCCATCATCTCTATTATCTTATGTTAAAGTATTTGAGGAAATGAG
                                                                                                                                                    TGGTATTTACAATGCACCTGTAGCCTTGTCAGTATATGCGAAGGTGTTTTGAAAAGGAAAA
                                                                                                                                                                                                TTTAGGAAGCGATACAGCTCCACATCTTCATAAAAATAAAATTAATATGCTTGGATGTGC
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                                                                                                                                                                                                                                                                         <u>AAAAAACAAACATCGAATGGCACTAAGAAAAGCCATCTCTAATGGAGATAAACATTTTTT</u>
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                                                        AGCGTTAAAATATTTACAATCTTTTTGTTCTGAAAATGGTCCTAAATTTTATAACATGCC
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Pred. No. 6.6e-71;
0; Mismatches 478;
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GAGCATATCACTACCGCCGATGCAGCGGATTTTTGTCTTGCT---CAAGGCAATCACATC

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; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 410
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-410
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US-09-540-236-410
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Patent No. 6673910

Patent No. 6673910

Patent No. 6673910

Patent No. 6673910

Patent No. 6673910

APPLICANT: GATY L. Breton et al.

APPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPPUTICS

FILE REFERENCE: 2709,2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.1%;
Best Local Similarity 55.3%;
Matches 552; Conservative
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     GAGCATGTTACCACCATTGATGCTGTTAAGTTTGTTGAATCTTGCACTGAAGGATTTGTT
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                                                            TTCATTGAAACGGTTCTAAGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTCGTGATG
                                                                                                        CTACTGGTGCATGGTGAAATTACCGATAGCAACATTGATATCTTTGATCGTGAAAAAACGA
                                                                                                                                                                    ACTGATATTTTGGCACGCAGCTT---GGTATTTGAGGCCATGCAAAAGCATGGCATACCG
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                                                                                                                                CTGCTGGTTCATGGAGAGGTTACTAATCCTGAGGTTGACATGTTTTGATAGAGAAAAAGGTA
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Pred. No. 7e-66;
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US-09-252-991A-920
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US-09-252-991A-920
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PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142

RUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 10716,136
CURRENT FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 920
LENGTH: 1197
TYPE: NNA
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Best Local (
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ORGANISM: Pseudomonas
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255 ATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCT
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                                                                                                                                 CCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTCCT
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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US-09-596-002-36/c
; Sequence 36, Application US/09596002
; Patent No. 6632636
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US-09-596-002-36
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Best Local Similarity
Matches 549; Conserv
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FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
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                                                 gcagcaactercaccccacaacarcrrrrrrraaacaggaartcrcrcrccaaggggc
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GAGCATATCACTACCGCCGATGCAGCGGATTTTTTGTCTTGCT---CAAGGCAATCACATC
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Pred. No. 3.3e-63;
0; Mismatches 423;
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US-09-489-039A-418
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NO 418
LENGTH: 1059
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 418, Application US/09489039A
PATENT NO. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
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Local Similarity 54.4%;
nes 490; Conservative
                                                                                                 279 GCTGGAACGCGGCTTTAACGAAGGGTGTTCACCGCCGCCAAGCTCTACCCCGCCAATGC
                                                                                                                                260 AATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCTGGTGC 319
                        CACTACTAACTCCAGCCACGGCGTCACCAGCACCGACGCCA---TTATGCCAGTGCTGGA
                                                           CACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGTTCTACA
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1008
LENGTH: 1266
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1008
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US-09-252-991A-1008
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GENERAL INFORMATION:
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                                                                                                                                                      459 AAGGTATTCATTGAAACGGTTCTAAGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTC
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TTTGTTGCAGCAACTGTCACCCCACAACATCTTGTTTTGAACAGGAATTCTCTCTTCCAA 638
                                     GTCTTCGAGCACATCACCACCGGCCGACGCCCAGTTCGTCCGGGAAGCCCC---GGCC 118
                                                                      GTGATGGAGCATGTTACCACCATTGATGCTGTTAAGTTTTGTTGAATCTTGCACTGAAGGA 578
                                                                                                                 AAGCAGTTCÁTCGÁCGAGCACCTGCGCGCGGTGGTCGAGCGCTTCCCGGACCCTGÁAGGTG 61
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ilarity 52.9%;
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Best Local Sim
Matches 145;
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Patent No. 6551795
GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 963
LENGTH: 615
                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ARRIGINOSA FOR DIAGNOSTICS SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
THE OFFICE OF NOC. 11142
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Similarity 53.4%;
66; Conservative
        SEQ ID NOS:
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Pred. No. 2.7e-14;
0; Mismatches 145
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180 900 120

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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO C

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 4003

LENGTH: 1098
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Best Local Similarity
Matches 217; Conserv
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LENGTH: 294
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Best Local Similarity
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ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                            ORGANISM: Candida albicans
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                           TCTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAAAAGAGTGT---TCTTGTGGATG
                                                                                                                                                                                                              TGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCACAACATCTTGTTTTGAA
CTTTGGTTCTGATAGTGCGCCACATCCGATTCATGCAAAAGCAAACTCACGTTGGTGTGTG
                                                           GTTTCAAAAAGACAGAAAAGCACTTGTTGATGCTGCAACTAGTGGAGAACCATGGTTTTT
                                                                               AAGAGAGATCCACAGGGAGGCACTTGTGTCAGCTGTAACAAGTGGAAGTAAAAGATTTTT
                                                                                                                         CATTGAT-----AATTGGGCCGGAAATCCAATTAATTTTTGTAAACCAGTTGCCAA
                                                                                                                                                    CAGGAATTCTCTCTTCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCCAGTCCTCAA
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Pred. No. 1.1e-13;
0; Mismatches 179;
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US-09-806-708B-22/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial
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SYAHSYWYWSNNAMWYRRYSARNWSSMARWTTRNNWWMSGBVRMRWAGTMWWRHWNNNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence
US-09-806-708B-22
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SEQ ID NO 22
LENGTH: 1141
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Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic TI
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      932 VRRMAMKAKNINININÄYWTACYNRAATINIKMATHWMKWTHGAHSKRRTRHHTRTCRRTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 CCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGTTCTAC
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                                                                                                                                                           NTDARRTNNTTVMRRRWMTNTKTRWYSTTRRHHYTGATNNNNNNNNNNNNNNNNNNNSCCTCT
                                                                                                                                                                                                        TTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTG--TCACCCCACAACATCTTGTTTT
                                                                                                                                                                                                                                                                TWYWDMYTTMBTTTTRNWTTSTNWTNNNNNMWACTNNNNNNWWKAYYAHATNNWGCWWN
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                                                                                                  GAACAGGAATTCTCTCCTCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCCAGTCCT
                                                                                                                                                                                                                                                                                                              AATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTAAGTTTG
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                                                     RMMTMRWTMKGDGMTVRKKVKWRDTTCTYVDVWADSWVWWYANWMRCRDVTYTRNNTYCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 55.8; DB 4; 12.8%; Pred. No. 8.3e-07;
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RESULT 15
US-09-252-991A-962
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 962
LENGTH: 255
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAAATGCTCGACTGGTTG 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGCTGGTATTTACAATGCACCTGTAGCCTTGTCAGTATATGCGAAGGTGTTTGAAAAG 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTCTTGGGACTGATAGTGCTCC--TCATGATAGACGAAGAAAAGAGTGTTCTTGTGGA 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATATCCTTTCAGCTAATAAATTATGGAAACAATAA 1190
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                                                                                                                                                                                                                                                                                GCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAAG
                                                                                                                                                                                                                              AATACCGTCGGCGACGCCGCACCTTCGGCCGCGCATCGTCATGCCGAACCTGGTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                CTCTCAATCACAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTAAG
                                                                                                 CCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATATTGAAATCTTTA 194
                                                                                                                                                                                                                                                                                                                                                       CTCACCCTCCTGCGCCCCGACGACTGGCACATTCACCTGCGTGACGGTGCCGCGCGCCC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 51.2; DB 4;
52.9%; Pred. No. 9.5e-06;
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Db 228 CCCGCCGCCAGCCGCTTCGAGCCGCTGA 255

Search completed: February 12, 2005, 05:12:43 Job time : 263 secs

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Minimum DB seq length: 0
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Perfect score:
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                         Published Applications NA:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ן ד	DB .	ID	Description	
_	646	50.8		18	US-10-451-554-2		<u></u>
N	607.4	47.8	1826	17	US-10-424-599-6649	Sequence 6649, F	ΰ
ω	549.2	43.2	1545	18	US-10-437-963-86830	Sequence 86830,	Þ
4.	531.6	41.8	1893	18	US-10-425-115-86204	Sequence 86204, A	Þ
ហ	345	27.1	1258	18	US-10-425-115-86207	Sequence 86207, A	Þ
o	311.8	24.5	931	18	US-10-767-701-2040	Sequence 2040, Ap	ΰ
7	281	22.1	1053	17	US-10-282-122A-41490	Sequence 41490,	Þ
œ	277.2	21.8	1047	17	US-10-282-122A-42220	Sequence 42220,	×
9	267.4	21.0	1032	17	7 US-10-282-122A-8516	Sequence 8516, Ap	Ó
10	265.2	20.9	1056	17	US-10-282-122A-14242	Sequence 14242,	×
11	264.4	20.8	1092	17	US-10-282-122A-11985	Sequence 11985, A	Þ

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ALIGNMENTS

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APPLICANT: Rodolphe Arthur Kanhonou
APPLICANT: Ramon Serrano Salom
APPLICANT: Ramon Serrano Salom
APPLICANT: Roque Ros Palau
ITITLE OF INVENTION: Sugar beet genes involved in stress tolerance
FILE REFERENCE: 1187-24
CURRENT APPLICATION NUMBER: US/10/451,554
CURRENT FILING DATE: 2003-66-20
PRIOR APPLICATION NUMBER: ET/EP01/15093
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: EP 00870319.1
PRIOR APPLICATION NUMBER: EP 00870319.1
PRIOR APPLICATION NUMBER: US 60/271,656
PRIOR FILING DATE: 2001-02-26
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Best Local Simi
Matches 793;
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SEQ ID NO 2
LENGTH: 1743
TYPE: DNA
ORGANISM: Beta vulgaris
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193 GTAAAGATGGAACTGACTCTTACACGCCCTGATGACTGGCATCTACATCTCCGCGATGGA 252
                                3 GCAAAAATGGAGCTCTCAATCACACAACCTGATGATTGGCATCTTCATCTCCGTGATGGT 62
                                                                                                                                  Similarity
                                                                                                       Conservative
                                                                                                       50.8%; Score 646; DB 18; 76.4%; Pred. No. 5.2e-175; tive 0; Mismatches 245;
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RESULT 2
US-10-424-599-6649
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; Publication No. US20040031072A1
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GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

ITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

INVERIOR OF SEQ ID NOS: 285884

SEQ ID NO 6649

LENGTH: 1826

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

FEATURE:
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Best Local Similarity 74.3%;
Matches 778; Conservative
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LOCATION: (1)..(182
OTHER INFORMATION:
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                                                       CAGCATCTTCTGAATCGTAATGCTTTGTTCCAAGGTGGCTTACAGCCTCACAATTAC
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Pred. No. 7.2e-164;
0; Mismatches 268;
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RESULT 3
US-10-437-963-86830
US-10-437-963-86830, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
TA ROSE, Thomas J.
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APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andre
                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT4530_85834C.1
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                          Local Similarity
nes 734; Conserv
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Barbazuk, Brad
Li, Ping
                       TTTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTTGACAGATACAACCAG
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Pred. No. 4e-147;
0; Mismatches 308;
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RESULT 4
US-10-425-115-86204
US-10-425-115-86204
; Sequence 86204, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules a
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (53222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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                                                                                      Other Molecules
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; OTHER INFORMATION: Clone ID: MRT4577_178628C.1
US-10-425-115-86204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 86204
; LENGTH: 1893
; TYPE: DNA
ORGANISM: Zea mays
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Best Local Similarity
Matches 720; Conserv
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                                           AAAGGAAAATGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTTTA 910
                           AGAGGCTGGTGCCCTTGATAAACTAGAAGCATTTACAAGCTTCAATGGCCCTGATTTTTA
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Sequence 86207, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: LA ROSSA, Thomas J.

APPLICANT: Cao, Yihua

APPLICANT: Chou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REPERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 86207

LENGTH: 1258

TYPE: DNA
ORGANISM: Zea mays
FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_178630C.1
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US-10-425-115-86207
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Best Local Similarity
491 GGTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGT
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                                                                                                                                                                                                                                                                                        489 GCTGCCGGCAGGGAGTAGCTTCGAGCCGCTCATGACACTATACCTCACAGACAACAACAAG
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                                                                   TCCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTT
                                                                                                       GĠŦĊĊŦĊĠĀĠĠĀĠĀŦĠĠŦĊĄĠĠĊĀĠĠĀĀĀŦĠĊĊĠŦŦĠĊŦŦĠŦŦĊĀŦĠĠĀĠĀĀĠŦĊĀĊĄĠĀ
                                                                                                                           AGTTCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGTTACTAA
                                                                                                                                                                  TGCTGGAGCAACTÁCCAATTCCCAAGÁTGGTGTCÁCTGÁTATATTTGGGAAGTGCTTGCC
                                                                                                                                                                                     TGCTGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACC
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Pred. No. 2.7e-88;
0; Mismatches 230;
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US-10-767-701-2040
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Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT PILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 2040

LENGTH: 931
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Best Local &
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                              TCCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTT
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                                                                                                 AGTTCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGTTACTAA
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TCCACATGTTGACACCTTTGACCGTGAGAAGGTTTTCATTGACAAAATATTGGCACCACT
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Pred. No. 8.4e-79;
0; Mismatches 192; Indels 0;
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US-10-282-122A-41490
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41490
LENGTH: 1053
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Publication No. US20040029129A1
                                                                                                                              Matches
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                Local
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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                                                                                                                                               Similarity
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Zyskind, Judith
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Conservative
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Pred. No. 6.9e-70;
0; Mismatches 430;
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TITLE OF INVENTION: Identification of Essential Genes in PILE REFERENCE: ELITAA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/296,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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Best Local Similarity 55.9%;
Matches 569; Conservative
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                                         TTTGAACAAATGCAAAAGATAGGCATGCCCCTGCTTATTCACGGTGAGGTAACAGATGCG
                                                                        CTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGGTTACTAATCCT
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Carr, Grant
Topoto, Robert
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Forsyth, R.
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RESULT 8
US-10-282-122A-42220
Sequence 42220, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert 985 975 925 865 855 805 795 568 508 495 448 435 388 375 331 315 271 255 214 195 154 ATGCCGTTTGGCAGCGATATCGTGGTGCCAATCCGCGCCGGTGAAAATATCGAGTGG 94 TTTTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCGACTGG 1031 ĊŦAĊĊŦĊĠĊĀĀŦĊĀAGAGĀĊĊĠŦĊĀĊĠĊŦĊĀĊĊĀĀĠĊAAGĊĊŦĠĠĊĊAĠŦĊĠĊAĠĀĀAGĊ GAAGGTAAGCTAGAAÁTCTGGAAGCGTTCGCTAGCTTTÁATGGCCCTGÁTTTCTÁCGGC 924 GAAAATGCACTACGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTTTATGG 914 CTTCCTAGGAACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAATCC TGCGCAGGTTCTTÁCACAGCCCATGCAGCTCTTGAGTTGTÁTGCCGAAGTGTTTGAÁAAA TGTGCTGGTATTTACAATGCACCTGTAGCCTTGTCAGTATATGCGAAGGTGTTTGAAAAG rrcrrccradenácedacrerecedacedecanagedecedenándagecederiterese TTTTTTCTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAAAGAGTGTTCTTGTGGA ĊŦŖĀĀĠĊĠŦĠĊĠŔĊŦĊŔĊĊŖŖĊŔĊĠĊĠŦŦŖĠŦĠĠĊŔĠĊĠĠĊŔŔĊĊŦĊŦĠĠĊŔĠĊŔĸĠŖĸŖ CTCAAAAGAGAGATCCACAGGGAGGCACTTGTGTCAGCTGTAACAAGTGGAAGTAAAAGA TTTÄÄČCGTÄÄCCACATGCTGGTTĞGCĞĞTATTČGCČČAÇÄTTTCTÄĞTĞTTTĞÇÇÄATÇ TTTGTGCAA----CAAGCAGGCGATAACGTTGCGGCAACGATTACCGCGCACCATTTGCTG 624 TTTGTTGAATCTTGCAÇTGAAGGATTTGTTGCAGCAAÇTGTCACCCCACAACATCTTGTT 614 AATGATTTCCCGCAACTGAAAATTGTGCTTGAACACATCACCACCGCCGATGCAGTGACC CAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTAAG GAAGTCGACATTTTTGACCGTGAAAAGACCTTCCTAGACACCGTGCTTGCGCCGATCGTG GAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGTG GAĠĠĀĀĀŤTCGCAĀĀĠĊĊĀĀĀĠĊĠŦCAGGCAĀĀĠŤCGŤŤĠCAĞCTĀĀĠĊŤŦŤĀĊĊĊĀĠĊĊ ATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAGTTGTACCCTGCT ttgcaagcatgcaggaagtcggtatgttgctgttgttgctgcacggtaagtcaccacgcac CTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGTTACTAATCCT GGTGCGACCAACTCGGATTCAGGCGTCAC---TTCAGCCAAAAACATTTACCCAGTT GGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGGAAGTGTTTACCAGTT CC---ACAAGCGCACTTTGAACCTTTGATGGCGCTTTACCTCACCGATAACACATCACCT CCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGATACAACCAGTCCT CCCCCTGTAACCACCACTGAGATGGCCTTAGCCTATCGTGAGCGCATTATGGCCGCTCAG CCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGGCGATATTGAAATCTTTA GATACTGTACGCGACATCAGCCGTTATAACGGCCGCGCGCTGATCATGCCTAACACGGTT

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APPLICANT: XU, H:
APPLICANT: XU, H:
TITTE OF INVENTION: Identification of Essential Gen
FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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US-10-282-122A-8516
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Malone, Cheryl
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLING DATE: 2001-02-09
PRIOR APPLIATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 786.4
SOFTWARE: PatentIn version 3
SEQ ID NO 8516
LENGTH: 1032
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Best Local Similarity
Matches 540; Conserv
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                                                           ACTGATAGTGCTCCTCATGATAGACGAAGAAAAGAGTGTTCTTGTGGATGTGCTGGTATT
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                                                                                                                                                                                             TCTCTCTTCCAAGGGGGCTTACAACCGCATAATTACTGCCTTCCAGTCCTCAAAAGAGAG
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                                 ACAGACAGCGCTCCTCATGCACAAAATGCAAAAGAGAATGCTTGTGGATGTGCAGGCTGC
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Pred. No. 5.7e-66;
0; Mismatches 411;
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APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR APPLICATION NUMBER: 60/269,308
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SEQ ID NO 14242
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US-10-282-122A-14242
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                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Burkholderia mallei
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                      74 GGCAGTTGTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAA
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Malone, Cheryl
Haselbeck, Robert
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Sequence 11985, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
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US-10-282-122A-11985
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Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 11985
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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OR PILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/230,347
OR APPLICATION NUMBER: 60/230,347
OR APPLICATION NUMBER: 60/230,347
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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   TCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGTTACTAATCC
                                                         TGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGT
                                                                                                                                                                               GCCGGCCGGGATGACGTTCGAGCCGCTGATGACGCTGTACCTGACCGACAACACGCCGCC
                                                                                                         CGACGAAATCCGCCGCGCGCGAAAGCGGCTTCGTGCACGGCGTGAAGCTGTATCCGGC
                                      AGGCGCCACGACGAATTCCGACCATGGCGTCACCGATC---TCGCGAAATGTGCGAAGAC
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Malone, Cheryl
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Grant
To, Robert
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Pred. No. 4.3e-65;
0; Mismatches 411;
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RESULT 12 US-09-790-988-1

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                                                                         TGAAAAGGAAAATGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTT
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CTACGGGCTGCGCGCAGCGCCGAGACGGTCACGCTGCGCCCGCGAGCCGTGGGAACTGCC
                                                        cdácácddccdccdccchcdáchádchgdáádagrincdcdádcinic reddccdáinin
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GENERAL INFORMATION:

APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATAKABE, HIDEMI
APPLICANT: WATAKABE, HIDEMI
APPLICANT: WATAKABE, HIDEMI
APPLICANT: SAKAKI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
FULL REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER: OF SEQ ID NOS: 7
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                                                                                                                                              Query Match
Best Local Simi
Matches 564;
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                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                      LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera
                                                              368078 AATCATTAAACCTGATGATTGGCATGTTCATTTAAGAGACAATGAGATTTTAAATCAAGT
                      80
                                                                                                        20
                                                                                                                                                                    Similarity
TGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCATGCCAAATTTGAAGCCTCC
                                                                                      AATCACAACCTGATGATTGGCATCTTCATCTCCGTGATGGTGATGTTCTTAAGGCAGT
                                                                                                                                                20.8%; ilarity 54.0%; Conservative
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Pred. No. 2.2e-63;
0; Mismatches 478;
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RESULT 13
US-10-282-122A-7036
: Sequence 7036, Application US/10282122A
: Publication No. US20040029129A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Liangsu
                                                                                                                                                                                                       369095 AAGTGATTAAAAATCAAGAGTATTT
                                                                                                                                                                                                                                                                                                                                                                 AATTÄÄCÄÄAGAÄÄCCÄTAÄCAATAÄTCÄÄAÄAACCGTGTÄÄAATTATTAÄÄAAAATAAA
                                                                                                                                                                                                                                                TCCTCTCAGAATCATTTGTCATT
                                                                                                                                                                                                                                                                                TGTTGGAAGAAATGTGÁTTÁÍTTCCATTTTTATCAGGTGÁÁÁÍTTTTAAÁCTGGTCAATTGA
                                                                                                                                                                                                                                                                                                           TTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCGACTGGTTGCCGGC 1039

        ТАGGAACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAATCCTTTTC

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; ORGANISM: Escherichia
US-10-282-122A-7036
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CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-10-2-9
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-16
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; SEQ ID NO 7036
; LENGTH: 1047
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Best Local Similarity
Matches 547; Conserv
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APPLICANT: Forsyth, R.
APPLICANT: Ku, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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GAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGAGGGTTACTAATCCTGAGGTT
                                                                                                                                                   ATCAAACTAGCAAGAGAGCCAGGTCGTATTTGGGGTGAAGGTTGTACCCTGCTGGTGGCC
                                      ACCĂCTAACTCCAGCCACGGCGTGACGTCAATTGACGCAA---TCATGCCGGTACTTGAG
                                                                          ACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAGTGTTTACCAGTTCTACAA 380
                                                                                                                        CTGGÁGCGCGGÁTTTAACGAAGGCGTGTTCACCGCTGCAAAACTTTÁCCCGGCAAACGCA
                                                                                                                                                                                                         GGGCACGÁTTTCÁCCCCATTGÁTGÁCCTGTTÁTTTAÁCÁGÁTTCGCTGGATCCTÁATGÁG
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Trawick, John
Carr, Grant
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ilarity 54.1%;
Conservative
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Pred. No. 1.1e-59;
0; Mismatches 459;
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RESULT 14
US-10-282-122A-30305
JS-10-282-122A-30305
Sequence 30305, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Es;
FILE REFERENCE: ELITA.034A
CURRENT APPLICATION NUMBER: US/10/282,12:
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Rober
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Yamamoto, Robert
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PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PAPPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-2-22
PRIOR PRIOR DATE: 2000-2-26
PRIOR PRIOR DATE: 2001-02-09
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FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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Pred. No. 2.4e-58;
0; Mismatches 465;
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APPLICANT: Ohleen, Kari
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, Judith
APPLICANT: Yamamoro, Robert
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APPLICANT: Yamamoro, Robert
APPLICANT: Yamamoro, Applicant
CURRENT APPLICATION NUMBER: U9/10/282,122A
FILE REFERENCE: ELITRA, 034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/201,723
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,347
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-23
PRIOR PRICATION NUMBER: 60/257,636
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PRIOR APPLICATION 
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US-10-282-122A-15202
                                                                                                                                                                                                        SOFTWARE: PatentIn v
SEQ ID NO 15202
LENGTH: 1062
TYPE: DNA
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US-10-282-122A-15202
JSequence 15202, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                       Query Match
Best Local Similarity
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                                       18.7%;
                                Score 238.2; DB 17;
Pred. No. 1.5e-57;
                                                                                                                                                                                                                                                                                                                                                                        See
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                                                            Length 1062;
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                                                                                                              GAAATTCCGGCGGAGGTCGCGTTCGGCGATACGACCCTGGTGCCGCTGTCCGGCGGCGAG 1038
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Search completed: February 12, 2005, 07:01:22 Job time : 817 secs

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BQ516583.1
                                                                                                                                                                                                                                                                    Solanum tuberosum
                                                                                                                                 Seq primer: T3
                                                                                                                                                                                                                                                                           Solanum tuberosum (potato)
                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                          GI:21375452
                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 820)

1 (bases 1 to 820)

1 (bases 1, Mart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and KaramyCheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

Other ESTS: ESTS(2399)

Other ESTS: ESTS(2399)

Ocnatet: Robin Buell BQ516583 820 bp mRNA linear EST 07-MAR-2003 EST623998 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMIY71 5' end, mRNA sequence. Email: potato-array@tigr.org
This clone can be obtained from the Univer.
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/ The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues" [Footation of the control /organism="Solanum tuberosum" /mal_type="mRNA" /cultivar="Kennebec or Binjte" /db_xref="taxon:4113" /clone="STMIY71" /tissue_type="mixed tissues" /lab_host="SOLR" from the University of Arizona Genomics 20850, USA

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                  RESULT 2
CK252266
LOCUS
                                                                                                       ACCESSION
VERSION
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Matches 818; Conservative
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           CK252266
EST735903 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCBT81 5' end, mRNA sequence.
CK252266
CK252266.1 GI:39806092
EST.
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                AGACTGTAGGTGTATCATCTTTTCTTTCATGTTGATTAGA
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Pred. No. 1.1e-214;
0; Mismatches 2;
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library, normalized and full-length
POCBT81 5' end, mRNA sequence.
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Matches 771; Conserv
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ACAACATCTTGTTTTGAACAGGAATTCTCTCTTCCAAGGGGGCTTACAACCGCATAATTA
                                                 TGATGCTGTTAAGTTTGTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCC
                                                                                       AGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCAT
                                                                                                         AAGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCAT
                                                                                                                                                  GGTTACTAATCCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCT
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1 (bases 1 to 1007)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Generation of ESTs from potato callus tissue (2003)

Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                    GGTTACTAATCCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: potato-array@tigr.org
Clones can be requested from the University of I
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                       GIGITTACCAG
                                                                                                                                                                                                                               GTGTTTACCAGTTCTACAAGAAATGGTTGAGCATAATATGCCTCTGGTGGTTCATGGAGA 421
                                                                                                                                                                                                                                                                     grtgtaccctgctgctgccacgacaaattctcaagatggagtgactgatcttttcggaa
                                                                                                                                                                                                                                                                                        GTTGTACCCTGCTGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="potato callus cDNA library, full-length"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCBT81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="callus"
/lab_host="DH108-TonA"
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Pred. No. 5.4e
0; Mismatches
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                                                                                                                            751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Other ESTS: EST62398
Contact: Robin Buell
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamide; Solanales; Solanaceae; Solanum.

1 (bases 1 to 751)
Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses resulting a set of potato cDNA clones for microarray analyses
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BQ516584.1 GI:21375453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAAGTAAAAGATTTTTTTTTTGGGACTGATAGTGCTCCTCATGATAGACGAAGAAA
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GTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCACAACATCTTGTTTTG
                                                                                                                                                 GTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGTGCAG
                                                                           AAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATTGATGCTGTTAAGTTT
                                                                                                                            GGTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCTAAGACCGTTGGTGCAG
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                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                     /lab_host="SOLR"
/clone lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants; petioles, germinating eyes, tubers, or roots."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="mixed tissues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMIY71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Solanum tuberosum"
                                                                                                                                                                                                                   58.6%;
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Pred. No. 1e-194;
0; Mismatches 4;
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                                                                                                                                                            Eukaryota; Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 915)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue Unpublished (2003)

Other_ESTs: EST736836

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                          CK253198 915
EST736835 potato callus cDNA
Solanum tuberosum cDNA clone
CK253198
                                                                                            Email: potato-array@rigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/ .
Seq primer: ATT TAG GTG_ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                  Solanum tuberosum
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   /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp mRNA linear EST 30-JUL-2004
library, normalized and full-length
POCC351 5' end, mRNA sequence.
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Best Local Similarity
Matches 695; Conserv
                         CK242513 790 b

BST726150 potato callus cDNA 1

Solanum tuberosum cDNA clone p

CK242513

CK242513.1 GI:39786211

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           Solanum tuberosum (potato)
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                                                                                                                                                                                                                                                                                                                                                                                          GTTGTACCCTGCTGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                         GTTGTACCCTGCTGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAA 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATGTTCTTAAGGCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="potato callus cDNA library, normalized full-length"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4113"
/clone="POCC351"
/tissue_type="callus"
/lab_host="DH10B-TonA"
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Pred. No. 8.7e-180;
0; Mismatches 7;
                                                bp mRNA linear EST 30-JUL-2004
library, normalized and full-length
POCA005 3' end, mRNA sequence.
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                                                        GGCTCCTCTCTGAGAA--
              TTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCGACTGGTTGCC
                            TTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAATGCTCGACTGGTTGCC 1036
                                                                                                   AAATGCACTCGACAAGCTTGAAGCATTTACTAGCTTCAATGGACCAGACTTTTATGGGCT
                                                                                                                APATGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACCAGATTTTTATGGGCT
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                                                                                                                                                                                                                                                CAAAAGAGAGATCCACAGGGAGGCACTTGTGTCAGCTGTAACAAGTGGAAGTAAAAAGATT
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                                                                                                                                                                                                                                                                                                                                     TGTTGAATCTTGCACTGAAGGATTTGTTGCAGCAACTGTCACCCCCACAACATCTTGTTTT
                                                                                                                                                                                                                                                                                                                                                                 GAAATTTCCACAATTGAAGGTCGTGATGGAGCÁTGTTACCACCATTGATGCTGTTAAGTT
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95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 689.6; DB 7;
Pred. No. 1.8e-179;
0; Mismatches 9;
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Indels Length

Gaps

790; 22;

-TCATTIGTCATTCTTGTACTGT 1074

251

976 371 916 431 856 491 551

736 611 676

671 616 731 556

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Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamidis; Solanales; Solanaceae; Solanum.
1 (bases 1 to 790)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Other ESTs: EST726147 EST726148 EST726149
                                                                                                                                                                                                                                                                                                                                                                                                 Email: potato-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850,
                                                                                                                                                                   /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="texon:4113"
/clone="pocA005"
/tissue_type="callue"
/lab_host="DH10B-TonA"
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
                                                                                                                  /clone_lib="potato callus cDNA library, normalized full-length"
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480

421 600 361 540

481 660

720

601

780 541

899 661 840

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REFERENCE
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                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
712 Medical Center Dr. Rockville, MD 20850, USA
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/ .
Seq primer: ATT TAG GTG ACA CTA TAG.
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1 (bases 1 to 920)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CK250612
CK250612.1 GI:39802848
EST.
Solanum tuberosum (potato)
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920 bp mRNA linear EST 30-JUL-2004
EST734249 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCBH29 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAGATATTATCACGATGATAATATCCTTTCAGCTAATAAATTATGGAAACAATAAGCTT 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCACGGTCACCAAAGTGCTCCTGTATTCTGAAGATTT
                                                        GCCAAATTTGAAGCCTCCTATCACTACCACTGCTGCTGCTGCTGCTAGCATACCGGGAGGCGAT 181
                                                                                                                            TGATGTTCTTAAGGCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCAT 121
                                                                                                                                                                                                  TGCAAAAATGGAGCTCTCAATCACACACACCTGATGATTGGCATCTTCATCTCCGTGATGG
                                                                                                         TGATGTTCTTAAGGCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCAT
                                                                                                                                                                               TGCAAAAATGGAGCTCTCAATCACACAACCTGATGATTGGCATCTTCATCTCCGTGATGG
 ATTGAAATCTTTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGA
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Solanum tuberosum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="callus"
/lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="potato callus cDNA library, normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="POCBH29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _xref="taxon:4113"
                                                                                                                                                                                                                                                                    52.1%;
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                                                                                                                                                                                                                                                    Score 662.6; DB 7;
Pred. No. 5.6e-172;
0; Mismatches 4;
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Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Bake Generation of ESTs from potato callus tissue

L Unpublished (2003)

Other_ESTs: EST733415

Conteact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-arrayerigr.org
Clones can be requested from the University of Arizona Gen Institute via http://genome.arizona.edu/orders/.

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 GTTGTACCCTGCTGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum tuberosum (potato)
Solanum tuberosum
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                                                                                          /mol type="mRNA"
/cultivar="Kennebec"
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/clone_typetato callus cDNA library, normalized and
full-langth"
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                  organism="Solanum tuberosum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920
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Genomics

and

Baker, B

Genomics

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ACCESSION
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BST726147 potato callus cDNA 1

Solanum tuberosum cDNA clone pl

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1 (bases 1 to 723)
Buell, C.R., Hart, A., Zismann, V., Karamycheva
Generation of ESTs from potato callus tissue
Unpublished (2003)
Other_ESTs: EST726148 EST726149 EST726150
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850,
                            AACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAAGGTACCCGAATCCTTTTCTTAT
  TTTTGAGAAAGGGAAAAAGAGATTCTCCTTCTCATTTGTCATTCTTGTACTGTAATATTTG
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Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/
Seq primer: TGT AAA ACG ACG GCC AGT.
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ilarity 94.9%;
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/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="caxon.4113"
/clone="POCA005"
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/lab_host="DH10B-TonA"
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Pred. No. 3.7e-159;
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708 by RST735147 potato callus cDNA 1
Solanum tuberosum cDNA clone Pr
CK251510
CK251510.1 GI:39804606
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Solanum tuberosum (potato)
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Buell C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Generation of ESTs from potato callus tissue Unpublished (2003)
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Contract: Robin Buell
The Institute for Genomic Research
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                 GTACCCTT
                                               GTAGCCTTGTCAGTATATGCGAAGGTGTTTGAAAAGGAAAATGCACTCGACAAGCTTGAA 878
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/mol_type="mRNA"
/cultivar="Kennebec"
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/lab_host="DH10B-TonA"
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/clone="POCBN96"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Contact: CUGI
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van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fri Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, 3-8 mm bus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
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     /clone="c:vo-x---
/tissue_type="flower"
/dev stage="3-8mm buds"
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; The
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research. Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TAA96).
They were immediately frozen in liquid nitrogen and ther
                                                                                                                                                                                                                                                                                       organism="Lycopersicon
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                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                       /db_xref="taxon:4081"
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3 - 8 mm buds Lycopersicon
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CNSOA31G 1301 bp mRNA linear HTC Arabidopsis thaliana Full-length cDNA Complete sequence GSLTPCH90ZE05 of Hormone Treated Callus of strain col-0 Arabidopsis thaliana (thale cress)...
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                                                                                                                                                AAGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCAT
                                                                                                                                                                                    Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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nilarity 99.0%;
Conservative
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/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: No supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
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/cultivar="Kennebec"
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GI:42460819
BX828451.1 GI:42460819
HTC; GSLT cDNA.
ArabidopsIs thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) of full-length librairies construction: Temple
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Location/Qualifiers
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                                                                                                                                                                                                CCAAATTTGAAGCCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGATA 182
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   TTGTACCCTGCTGCTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAAG
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                                                                    ACAACCAGTCCTATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAAG
                                                                                                       <u>AAAACTCTACCTGAAGAGATCAGGCTTGCAAGGGAAAGTGGTGTGGTTTATGCGGTGAAG</u>
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larity 72.9%;
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/clone="GSITPGH90ZE05"
/tissue_type="Hormone Treated Callus"
/plasmid="pCMVSPORT_6"
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/strain="Col-0"
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Pred. No. 1.5e-150;
0; Mismatches 281;
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CTTCAATGGCAACCG 1221
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                                                                      GTTCCAGACGTTTTCAACTTCCCATTCGGAGAGATCGTCCCTATGTTTGCTGGAGAAACC
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RESULT 13
CNSOA38S
LOCUS
DEFINITION REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM

A Combined Approach Annotation

TOBIGE; CLUCY, J. M., Jaillon, O., Wincker, P., Clepet, C., Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Schachter, V., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Meissenbach, J. and Salanoubat, M. Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: Whole Genome Sequence Comparisons and Improve Arabidopsis Genome CNSOA38S

1294 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB93ZB09 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Arabidopsis thaliana (thale Arabidopsis thaliana BX827082.1 GI:42461050 GSLT_cDNA.

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Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
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                      AGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCATT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Direct Submission
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/clone="GSLTFB93ZB09"
/tissue_type="Flowers a
/plasmid="pCMVSPORT_6"
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72.8%;
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Pred. No. 4.2e-150;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1297)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetter, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:

Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:

Mole Genome Sequence Comparisons and Improve Arabidopsis Genome Arabidopsis thaliana (thale Arabidopsis thaliana Unpublished HTC; GSLT cDNA. BX828087.1 GI:42460698 cress)

Direct Submission

Direct Submission

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre Natio

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqre

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) mem

full-length librairies construction : Temple G.

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V., Aury J.M., Jaillon O., Wincker P., Menard M.

Schachter V., Weissenbach J., Salanoubat M.

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Annotation is based on the June 2003 version of

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/clone="GSLTPGH50ZG03"
/tissue_type="Hormone Tr
/plasmid="pCMVSPORT_6"
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/strain="Col-0"
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                                                               232
                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asterids; lamiids; Solanales; Solanaceae; Solanum.

(bases 1 to 792)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A.

Generation of ESTs from potato callus tissue

Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK251764 792 bp mRNA linear EST 30-JUL-2004 EST735401 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCBP96 5' end, mRNA sequence. CK251764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: potato-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/
Seg primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu asterids; lamiids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATTTCTATGGCCTTCCGAGAAACTCGTCAAAGATCACACTGAAGAAATCTCCTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATTTTTATGGGCTTCCTAGGAACAACTCAAAGATTAAGTTGAGTAAGACGCCATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCTTTGATGAGGCGGGTGCGCTGGACAAGTTGGAAGCTTTCACCAGTTTCAATGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGTTTGAAAAGGAAAATGCACTCGACAAGCTTGAAGCATTCACTAGCTTCAATGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTCTTGTGGATGTGCTGGTATTTACAATGCACCTGTAGCCTTG-TCAGTATATGCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTACCCGAATCCTTTTCTTATGCATCAGGAGATATTATTCCCATGTTTGCTGGTGAAAT
                                                               TGCAAAAATGGAGCTCTCAATCACACAACCTGATGATTGGCATCTTCATCTCCGTGATGG
         TGATGTTCTTAAGGCAGTTGTCTCTCACAGTGCACATCACTTTGGGAGGGCAATAGTCAT
                                                                                                                                             Conservative
                                                                                                                                                                                                                                    /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: supplier: RNA was isolated from Solanum tuberosum v. Kennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                                                                              full-length"
                                                                                                                                                                                                                                                                                                                                 /tissue_type="callus"
/lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4113"
/clone="POCBP96"
                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Solanum tuberosum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                             clone_lib="potato callus
                                                                                                                                                            100.0%;
                                                                                                                                             0
                                                                                                                                                            Score 561; DB 7; L
Pred. No. 7.5e-144;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                   cDNA library,
                                                                                                                                             0;
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772 TGATGCTGTTAAGTTTGTTGA 792	542 TGATGCTGTTAAGTTTGTTGA 562		482 AAGACCGTTGGTGCAGAAATTTCCACAATTGAAGGTCGTGATGGAGCATGTTACCACCAT 541	652 GGTTACTAATCCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCT 711	422 GGTTACTAATCCTGAGGTTGACATGTTTGATAGAGAAAAGGTATTCATTGAAACGGTTCT 481	592 GTGTTTACCAGTTCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGA 651	362 GTGTTTACCAGTTCTACAAGAAATGGTTGAGCATAATATGCCTCTGCTGGTTCATGGAGA 421	532 GTTGTACCCTGCTGGTGCCACGACAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAA 591	302 GTTGTACCCTGCTGGTGCCACGACAAATTCTCAAGATGGAGTGACTGATCTTTTCGGGAA 361	472 TACAACCAGTCCTATGGAAATCAAACTAGCAAGAGAGAGCCAGGTCGTATTTGGGGTGAA 531	242 TACAACCAGTCCTATGGAAATCAAACTAGCAAGAGAGAGA	412 ATTGAAATCTTTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTTGACAGA 471	182 ATTGAAATCTTTACCTGTTGATAGTGATTTCAACCCTCTTATGACACTTTATTGACAGA 241		122 GCCAAATTTGAAGCCTCCTATCACTACCACTGCTGCTGCTGTAGCATACCGGGAGGCGAT 181

Search completed: February 12, 2005, 05:08:17 Job time : 4627 secs